

; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 55
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(761)
US-09-796-753-55

Query Match
Best Local Similarity 87.7%; Score 755.2; DB 10; Length 969;
Matches 757; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 102 GGAGATCAGCGAGCTGGAGTTTCTTCAGATCATCATCGTGGTGGTGCATGATGAT 161
Db 2 GGAGATGGCGAGCTGGAGTTTCTTCAGATCATCATCGTGGTGGTGCATGATGAT 61

Qy 162 GGTGGTGGTGCATCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 221
Db 62 GGTGGTGGTGCATCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 121

Qy 222 CCGGCACAGCGAGCGGAGGAGAGAGATGCTCTCAGAGAGGATGCTGGGCC 281
Db 122 CCGGCACAGCGAGCGGAGGAGAGAGATGCTCTCAGAGAGGATGCTGGGCC 181

Qy 282 CTCGGAGACACAGTGTACGCAACCGAATCCAGAGCGCGAGTTCAGCCCGCTCG 341
Db 182 CTCGGAGACACAGTGTACGCAACCGAATCCAGAGCGCGAGTTCAGCCCGCTCG 241

Qy 342 GCCACCGAGCGCTGGCGCTGGCGCTTCGCCCGAGCGGAGCGTTCACCGCTTCCA 401
Db 242 GCCACCGAGCGCTGGCGCTGGCGCTTCGCCCGAGCGGAGCGTTCACCGCTTCCA 301

Qy 402 GCCACCTATCCGTACCTGCAGCAGCAGATCGACCTGCCACCCACCATCTTCGTG 461
Db 302 GCCACCTATCCGTACCTGCAGCAGCAGATCGACCTGCCACCCACCATCTTCGTG 361

Qy 462 CGGGAGAGCGCCCGCCCTACAGGCGCCCTGCACCTCAGCTTCGGGACCCCGAGCA 521
Db 362 CGGGAGAGCGCCCGCCCTACAGGCGCCCTGCACCTCAGCTTCGGGACCCCGAGCA 421

Qy 522 GCAGCTGGAACTGAACCGGAGTGGTGGCGGACCCCGGCAACAGAACCATCTTCGAC 581
Db 422 GCAGCTGGAACTGAACCGGAGTGGTGGCGGACCCCGGCAACAGAACCATCTTCGAC 481

Qy 582 TGACCTGATGATAGTGCAGGCTGGCGGCGCCCTGCCCGCCCGAGCAGTAACCTCG 641
Db 482 TGACCTGATGATAGTGCAGGCTGGCGGCGCCCTGCCCGCCCGAGCAGTAACCTCG 541

Qy 642 CAGCGCACAGTGTACGCGAGCGGCGGCGATGAGGGGCGCGCGCCACCTACAGCGA 701
Db 542 CAGCGCACAGTGTACGCGAGCGGCGGCGATGAGGGGCGCGCGCCACCTACAGCGA 601

Qy 702 GGTATCGGCGCACTACCGGGGTCTCTTCCAGCACAGCAGAGTGGCGCGCCCTC 761
Db 602 GGTATCGGCGCACTACCGGGGTCTCTTCCAGCACAGCAGAGTGGCGCGCCCTC 661

Qy 762 CTTCTCGAGGGAGCGCGGCTCCACACACACATCGCGCCCTCAGAGAGCGAGCAT 821
Db 662 CTTCTCGAGGGAGCGCGGCTCCACACACACATCGCGCCCTCAGAGAGCGAGCAT 721

822 CTCGAGCAAGAGAGGATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 861
722 CTCGAGCAAGAGAGGATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 761

RESULT 8
US-10-205-823-412
; Sequence 412, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endegs, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Womsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 412
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-412

Query Match
Best Local Similarity 87.6%; Score 754.2; DB 15; Length 1141;
Matches 762; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 87 TTTGTTCCAGAGCATGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGT 146
Db 77 TCTCTCGAAACAGGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCATCGTGT 136

Qy 147 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 206
Db 137 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 196

Qy 207 ACGGTCTTTCATCAGCGGACAGCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 266
Db 197 ACGGTCTTTCATCAGCGGACAGCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 256

Qy 267 AGGATGCTGTGGCCCTCGGAGAGACAGTGTACGAGCAACCGAATCCAGAGCGCAGGT 326
Db 257 AGGATGCTGTGGCCCTCGGAGAGACAGTGTACGAGCAACCGAATCCAGAGCGCAGGT 316

Qy 327 CTACGCCCGGCTCGGCCACCGAGCCGCTGGCGTGGCGCCCTCGGCCAGCGGAGCG 386
Db 317 CTACGCCCGGCTCGGCCACCGAGCCGCTGGCGTGGCGCCCTCGGCCAGCGGAGCG 376

Qy 387 CTTCCACCGCTTCAGAGCCCACTATCCGTACCTGCAGACGAGATCGACCTGCCACCCAC 446
Db 377 CTTCCACCGCTTCAGAGCCCACTATCCGTACCTGCAGACGAGATCGACCTGCCACCCAC 436

QY 646 GCCAGTCTACGACAGCGGGGCGCATGAGGGGCGCGCCACCTACAGGAGTC 705
Db 541 GCCACGTCTACGACAGCGGGGCGCATGAGGGGCGCGCCACCTACAGGAGTC 600
QY 706 ATCGGCCACTACCGGGGCTCTCTTCCAGCACAGCAGAGCAGTGGGGCGCCCTCTTG 765
Db 601 ATCGGCCACTACCGGGGCTCTCTTCCAGCACAGCAGAGCAGTGGGGCGCCCTCTTG 660
QY 766 CTGAGGGGACCGGGCTCCACACACACATCGGCCCTTAGAGGCGGAGCAGCATCTGG 825
Db 661 CTGAGGGGACCGGGCTCCACACACACATCGGCCCTTAGAGGCGGAGCAGCATCTGG 720
QY 826 AGCAAGAGAGAGGATAAAGAGGAGGACACCTCTC 861
Db 721 AGCAAGAGAGGATAAAGAGGAGGACACCTCTC 756

RESULT 14
US-10-241-220-45
; Sequence 45, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frazz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 45
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-241-220-45

Query Match 87.4%; Score 752.6; DB 15; Length 806;
Best Local Similarity 98.2%; Pred. No. 2.8e-189;
Matches 761; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 87 TTGTTCAGAGATGGAGATCAGGAGCTGAGTTTGTTCAGATCATCATCGTGT 146
Db 14 TCTCTCGAAACACGAGATGGGAGCTGGAGTTTGTTCAGATCATCATCGTGT 73
QY 147 GGTGATGATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 206
Db 74 GGTGATGATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 133
QY 207 ACGGTCTTTCATAGCCGACAGCCAGGGGCGGAGGAGAGATGCTCTGCTCAGA 266
Db 134 ACGGTCTTTCATAGCCGACAGCCAGGGGCGGAGGAGAGATGCTCTGCTCAGA 193
QY 267 AGATGCTGTGGCCCTCGAGAGCAGTGTGTCAGGACGGAATCCCGAGCCGAGT 326
Db 194 AGATGCTGTGGCCCTCGAGAGCAGTGTGTCAGGACGGAATCCCGAGCCGAGT 253
QY 327 CTACGCCCGCCCTCGGCCACCGACCGCTGCGCGCTGCGCCCTGCGCCAGCGGAGCG 386
Db 254 CTACGCCCGCCCTCGGCCACCGACCGCTGCGCGCTGCGCCCTGCGCCAGCGGAGCG 313
QY 387 CTTCACCGCTTCAGCCACCTATCGGTACCTGACGACGAGATGACCTCCACCCAC 446
Db 314 CTTCACCGCTTCAGCCACCTATCGGTACCTGACGACGAGATGACCTCCACCCAC 373
QY 447 CATCTCGTCTCAGAGCGGAGGAGCCCGCCACCTACAGGGCCCTGACACCTCCAGT 506

Db 374 CATCTCGCTGTACAGCGGGGAGGAGCCCGCCACCTACAGGGGCGCCCTGACCTCCAGCT 433
QY 507 TCGGACCCCGGACGAGCAGCTGGAACTGAACCGGAGTTCGGCGCAGACCCCAAAACAG 566
Db 434 TCGGACCCCGGACGAGCAGCTGGAACTGAACCGGAGTTCGGCGCAGACCCCAAAACAG 493
QY 567 AACCATCTTCGACAGTACCTGATAGTGCACAGGTTGGGCGGCGCCCTGCGCCCGCCAG 626
Db 494 AACCATCTTCGACAGTACCTGATAGTGCACAGGTTGGGCGGCGCCCTGCGCCCGCCAG 553
QY 627 CAGTAACCTCGGCATCAGGCGCAGCTGCTACGGGAGCGGCGGCGCATGGAGGGGCGCC 686
Db 554 CAGTAACCTCGGCATCAGGCGCAGCTGCTACGGGAGCGGCGGCGCATGGAGGGGCGCC 613
QY 687 GCCACCTACAGCAGGTCATCGGCACTACCGGGGCTCTCTTTCAGACGACGACAG 746
Db 614 GCCACCTACAGCAGGTCATCGGCACTACCGGGGCTCTCTTTCAGACGACGACAG 673
QY 747 CAGTGGGCGCCCTCTCTGCTGGAGGGAGCCCGGCTCCACACACACATCGCGCCCT 806
Db 674 CAGTGGGCGCCCTCTCTGCTGGAGGGAGCCCGGCTCCACACACACATCGCGCCCT 733
QY 807 AGAGAGCGCAGCCATCTGGAGCAAAAGAGAGATAAACAGAAAGACACCTCTC 861
Db 734 AGAGAGCGCAGCCATCTGGAGCAAAAGAGAGATAAACAGAAAGACACCTCTC 788

RESULT 15
US-10-098-841-71
; Sequence 71, Application US/10098841
; Publication No. US20020197679A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Aeundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Dmanac, Radje T.
; TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2
; CURRENT APPLICATION NUMBER: US/10/098,841
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 71
; LENGTH: 1066
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(867)
US-10-098-841-71

Query Match 86.2%; Score 742.4; DB 14; Length 1066;
Best Local Similarity 99.2%; Pred. No. 1.5e-186;
Matches 746; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 11, 2004, 21:06:02 ; Search time 390.646 Seconds

(without alignments)
9363.200 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861

Sequence: 1 atgcaccgttgatgggggt.....aacagaaaggacacctctc 861

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002s.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	861	100.0	1321	6	ABK12137 Human cDN
2	861	100.0	4839	7	ACC49552 Tumour-as
3	859.4	99.8	1383	9	ADC37326 Nuclear f
4	755.2	87.7	989	3	AAA75151 CDNA enco
5	754.2	87.6	1140	6	ABK92120 Prostate
6	754.2	87.6	1141	9	ADB75598 Prostate
7	754.2	87.6	1850	7	ACC49536 Tumour-as
8	753.6	87.5	969	3	AAA75164 CDNA clon
9	753.6	87.5	969	3	AAA75163 CDNA clon
10	753.6	87.5	969	3	AAA75165 CDNA clon
11	753.6	87.5	1140	9	AAD60105 Human and
12	752.6	87.4	806	7	ACC49537 Tumour-as
13	752.6	87.4	1061	3	AAA74729 Sequence
14	752.6	87.4	1085	9	ADC37324 Nuclear f
15	752.6	87.4	1334	7	ABZ36103 Human sec
16	742.4	86.2	1066	4	AAI57868 Human pol
17	712	82.7	1069	4	AAI59654 Human pol
18	612.4	71.1	878	6	ABK12142 Mouse cDN
19	544.4	63.2	1583	6	ABS61424 Prostate
20	462.2	53.7	1713	3	AAA75152 CDNA enco
21	460.6	53.5	1713	3	AAA75167 CDNA clon
22	460.6	53.5	1713	3	AAA75166 CDNA clon
23	460.6	53.5	1713	3	AAA75168 CDNA clon

C	24	445.6	51.8	693	6	ABK12143	Abk12143 Human MIV
	25	417.4	48.5	812	2	AAS25964	Aaz52964 Human pro
C	26	417	48.4	474	7	ABZ84732	Abz84732 Toxicolog
	27	401.4	46.6	408	5	AAF65983	Aaf65983 Novel hum
	28	400.6	46.5	673	6	ABT09178	Abt09178 Phase-1 R
	29	352.2	40.9	8494	5	AAS77304	Aaz52507 Human sec
	30	351.6	40.8	937	3	AAS77304	Aaz52507 Human sec
	31	350	40.7	920	6	ABK34251	Abk34251 Human cDN
	32	350	40.7	2170	7	ADA52629	Ada52629 Human cod
	33	349	40.5	8065	2	AAV38335	Aav38335 Manic-dep
	34	349	40.5	8093	6	ABK12145	Abk12145 Human MIV
	35	341.8	39.7	475	6	ABK12144	Abk12144 Human MIV
C	36	333.8	38.8	8103	5	AAS77312	Aas77312 DNA enco
	37	320.4	37.2	1879	5	AAS84503	Aas84503 DNA enco
	38	284.2	33.0	1496	9	ADC37452	Adc37452 Nuclear f
	39	284.2	33.0	8440	5	AAS77305	Aas77305 DNA enco
	40	284.2	33.0	8440	6	ABK83477	Abk83477 Human cDN
	41	281	32.6	8011	2	AAV38336	Aav38336 Manic-dep
	42	252.6	29.3	8041	5	AAS77310	Aas77310 DNA enco
	43	232	26.9	254	3	AAA41265	Aaa41265 Human sec
	44	223.4	25.9	1428	5	AAS92497	Aas92497 DNA enco
	45	223.4	25.9	2942	5	AAS77313	Aas77313 DNA enco

ALIGNMENTS

RESULT 1
ABK12137
ID ABK12137 standard; cDNA; 1321 BP.
XX
AC ABK12137;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.
XX
KW Human; ss; Gene; MIVR-1; Mechanically Induced Vascular Receptor 1;
KW Cytostatic; cardiac; cerebroprotective; antiarteriosclerotic;
KW Cardiac cell; anti-apoptotic; vascular endothelial cell;
KW Cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis;
KW heart failure.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 413..1276
FT /*tag= a
FT /product= "MIVR-1"
FT /note= "This region is specifically claimed in claim 3"

WO200216416-A2.
28-FEB-2002.
21-AUG-2001; 2001WO-US026089.
22-AUG-2000; 2000US-0227159P.
(BGHM) BEIGHAM & WOMENS HOSPITAL INC.
(PFIZ) PFIZER INC.
Lee RT, Landschulz KT, Kennedy SP, Thompson JP, Turi TG;
WPI; 2002-280912/32.
P-PSDB; AAU78231.
Novel nucleic acid molecule encoding Mechanically Induced Vascular Receptor-1 polypeptide, useful for treating cardiovascular diseases.
Claim 2; Page 87-88; 105pp; English.
The invention relates to an isolated nucleic acid molecule encoding a

Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having cardiac cell anti-apoptotic activity and fragments of it provided they are not identical to Genbank sequences A176141.1, A159439.0, NM_004338 and A0177461. Also included are expression vectors, host cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity with a candidate agent, where the molecule is a nucleic acid molecule comprising MIVR-1, Irfx-1, VDUP-1, BFG-2 and Irfx-1 or its expression product, determining if the anti-apoptotic activity is modulated and thereby identifying a modulator. The cardiac cell anti-apoptotic molecules and nucleic acids of the invention are useful for treating, diagnosing and monitoring progression of such diseases and disorders as characterised by increased apoptotic cell-death of vascular endothelial cells e.g. cardiac hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart failure. The present sequence encodes human MIVR-1

Sequence 1321 BP: 223 A; 493 C; 440 G; 165 T; 0 U; 0 Other;
xx
SQ

		Query Match	100.0%; Score 861; DB 6; Length 1321;
		Best Local Similarity	100.0%; Pred. No. 1.8e-167;
		Matches	861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	ATGCACCGCTTGATGGGGTCAACAGCACCGCCGCCGCCGCCGGCAGCCCATGTC	60
Dd	413		
QY	61	TCTGTCACGTGCAACTCAACAACGCTCTTTTCTCCAGACATGGAGATCA CGAGCTGGAG	120
Dd	473		
QY	121	TTTTGTT CAGATCATCATCTGTTGGTGGTAGATGGTGA TGTGTTGTTGATCA GTGC	180
Dd	533		
QY	181	CTGCTGAGCCACTACAAGCTGTCTGCA CGTCTT CATTCAGCCG GCACACCAGGGGCGG	240
Dd	593		
QY	241	AGGAGAAGATGCCCTGTCTCAG AAGATG CCTGTGG CCCTCGGAGAC ACGTGTCA	300
Dd	653		
QY	301	GGCAACGGAA TC CAGAGCGC AGGTCTAG CCCCCG CTGGCC CCA CGGACCG CTCGGC	360
Dd	713		
QY	361	GTGCGGCCCTTGCCCAGCGGGAGCGCTTC AC CGCTTC CAGGCCA CTA TCGGTACCTG	420
Dd	773		
QY	421	CAGCAGAGATCG ACTTGCCA CCCAAC ATCTCG CTGT CAGCGGGAGGAGCCCCACCC	480
Dd	833		
QY	481	TACCAGGGCCCTGC ACCCTCCAGCTTC GGGA CCCC GAGCAGCAGCTGG AAC TGAACCGG	540
Dd	893		
QY	541	GAGTCTGGTCGCGC ACCCCC AAA CAGAA CCA TCTTC GA CAGTGA CTTGATGGATG GCC	600
Dd	953		
QY	601	AGGCTGGGCGGCCCTG CCCCC CAGCAG TAACTCTGGGCATCAGCGCCACGTGCTACGGC	660
Dd	1013		
QY	661	AGCGCGCGGCATG GAGGGGCGCCGCC CCA CACTACAGCAGAGGTCA TCGGCCACTACCCG	720
Dd	1073		
QY	721	GGGTCTCTCTTCAG ACA CCA CAGAGCAG TGGGCGGCCCTCTTGTCTGGAGGGGACCCGG	780
Dd	1133		
Dd			

QY	781	CTCCACCACACACACATCGCGCCCTAGAGAGCGGACGCAATCTGAGCAAGAGAT	840
DB	1193	CTCCACCACACACACATCGCGCCCTAGAGAGCGGACGCAATCTGAGCAAGAGAT	1252
QY	841	AAACAGAAAGGACACCCCTCTC	861
DB	1253	AAACAGAAAGGACACCCCTCTC	1273
RESULT 2			
ACC49552	ID	ACC49552 standard; cDNA; 4839 BP.	
AC	XX	ACC49552;	
AC	XX		
DT	XX	01-JUL-2003 (first entry)	
DE	XX	Tumour-associated antigenic target protein TAT379 SEQ ID NO:119.	
KW	KW	Human; tumour-associated antigenic target; TAT; tumour; diagnosis;	
KW	KW	cancer; gene; ss.	
OS	XX	Homo sapiens.	
PN	XX	WO2003024392-A2.	
PN	XX	27-MAR-2003.	
PD	XX		
PF	XX	11-SEP-2002; 2002WO-US028959.	
PR	XX	18-SEP-2001; 2001US-0332268P.	
PR	XX	19-OCT-2001; 2001US-0339227P.	
PR	XX	07-NOV-2001; 2001US-0336827P.	
PR	XX	20-NOV-2001; 2001US-0331906P.	
PR	XX	02-JAN-2002; 2002US-0345444P.	
PR	XX	03-APR-2002; 2002US-0369724P.	
PR	XX	19-AUG-2002; 2002US-0484809P.	
PA	XX	(GETH) GENENTECH INC.	
PI	XX	Frantz G, Hillan KJ, Phillips HS, Polakis P, Spencer SD;	
PI	XX	Williams PM, Wu TD, Zhang Z;	
PI	XX	WPI; 2003-354551/33.	
DR	XX	P-PSDB; ABP97234.	
PT	XX	New antibodies against tumor-associated antigenic target polypeptide,	
PT	XX	useful for treating or diagnosing tumors or cancers in mammals, e.g.	
PT	XX	prostate cancer, lung cancer, prostate adenocarcinomas or renal cell	
PT	XX	carcinomas.	
PS	XX	Claim 2; Fig 119; 285pp; English.	
CC	XX	ACC49493 to ACC49552 encode the human tumour-associated antigenic target	
CC	XX	(TAT) proteins given in ABP97175 to ABP97234. The present invention	
CC	XX	describes an isolated antibody that binds to a polypeptide having at	
CC	XX	least 80 % sequence identity to any of the 60 150-800 residue amino acid	
CC	XX	sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking	
CC	XX	its associated signal peptide, encoded by any of the 60 2000-3000 base	
CC	XX	pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have	
CC	XX	cytostatic activity. The antibody can be used for treating or diagnosing	
CC	XX	tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast	
CC	XX	cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal	
CC	XX	cell carcinomas, or thyroid cancer	
SQ	XX	Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;	
Query Match 100.0%; Score 861; DB 7; Length 4839;			
Best Local Similarity 100.0%; Pred. No. 2.le-167;			
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
QY	1	ATSCACCGTTCATGGGGTCAACAGACACGCCCGCCCGCGGAGCCCAATGTC	60

Qy

Db 741 CAGCAGGATCGACCTCGCGCCACCACATCTCGCTGTTCAGACGGGGAGGAGCCGCCACCC 800
Qy 481 TACCAGGCGCCCTGACCTCTGAGCTTCGGGACCCCGAGCAGCAGCTGGACTGAACGG 540
Db 801 TACCAGGCGCCCTGACCTCTGAGCTTCGGGACCCCGAGCAGCAGCTGGACTGAACGG 860
Qy 541 GAGTCGGTGGCGGACCCCGCCAAAGAACCAATCTTCGACAGTGCCTGATGATGATGCC 600
Db 861 GAGTCGGTGGCGGACCCCGCCAAAGAACCAATCTTCGACAGTGCCTGATGATGATGCC 920
Qy 601 AGGCTGGGGCGCCCTGCGCCCGCCAGCAGTAACTCGGCGATCAGCGCCACGCTGATGCC 660
Db 921 AGGCTGGGGCGCCCTGCGCCCGCCAGCAGTAACTCGGCGATCAGCGCCACGCTGATGCC 980
Qy 661 AGCGCGGGCGCATGAGGGGCGCGCCCGCCACCTACAGCAGGTCATCGGCCATACCCG 720
Db 981 AGCGCGGGCGCATGAGGGGCGCGCGCCCGCCACCTACAGCAGGTCATCGGCCATACCCG 1040
Qy 721 GGGTCTCTTCCACACACGAGCAGTGGCGCCCTCTGCTGGGGGACCCGG 780
Db 1041 GGGTCTCTTCCACACACGAGCAGTGGCGCCCTCTGCTGGGGGACCCGG 1100
Qy 781 CTCACCCACACATCGCGCCCTAGAGAGCGGAGCAGCAGTCTGAGCAAGAGAGGAT 840
Db 1101 CTCACCCACACATCGCGCCCTAGAGAGCGGAGCAGCAGTCTGAGCAAGAGAGGAT 1160
Qy 841 AAACGAGAGGACACCTCTC 861
Db 1161 AAACGAGAGGACACCTCTC 1181

RESULT 4
ID AAA75151 standard; cDNA; 969 BP.
XX
AC AAA75151;
XX
DT 15-JAN-2001 (first entry)
XX
XX cDNA encoding a human TANGO 261 polypeptide.
DE
XX TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
KW cellular proliferation; cellular differentiation; cellular adhesion;
KW von Willebrand factor-associated disorder; cell trafficking; cancer;
KW hematopoietic associated disease; atelectasis; pulmonary congestion;
KW oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
KW intestinal disorder; spleen associated disease; renal disorder;
KW cardiovascular disorder; ischemic heart disease; hydrocephalus;
KW brain herniation; iatrogenic disease; inflammation; meningitis;
KW Alzheimer's disease; cerebral toxoplasmosis; Parkinson's disease;
KW multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
XX

OS Homo sapiens.
XX
XX
XX
FH Key Location/Qualifiers
CDS 6..764
FT /*tag= a
FT /product= "TANGO 261"
FT 6..89
FT sig_peptide /*tag= b
FT mat_peptide 90..764
FT /*tag= c
XX
XX WO200052022-A1.
XX
XX
XX 08-SEP-2000.
XX
XX 01-MAR-2000; 2000WO-US0005226.
XX
XX 01-MAR-1999; 99US-0122458P.
XX
XX (WILL-) MILLENNIUM PHARM INC.
XX

PI Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
XX WPI: 2000-579269/54.
DR P-PSDB; AAB18449.
XX
PT Novel human and murine secreted proteins designated TANGO 216, 261, 262,
PT 266 and 267 useful as modulating agents of cellular processes, e.g. for
PT treating cancer.
XX
XX Claim 2; Fig 5; 175pp; English.
XX
XX The present sequence encodes a human TANGO 261 polypeptide. The
CC specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO
CC 267. The TANGO polypeptides can be used to modulate cellular
CC proliferation, modulate cellular differentiation and/or modulate cellular
CC adhesion. The proteins can be used to treat any von Willebrand factor-
CC associated disorder, regulate extracellular matrix structuring, cellular
CC adhesion, and cell trafficking and/or migration, modulate cellular
CC interactions, modulate cell adhesion in proliferative disorders, such as
CC cancer, modulate the proliferation, differentiation, and/or function of
CC cells that appear in the bone marrow, and leukocytes, treat bone marrow,
CC blood and hematopoietic associated diseases and disorders, atelectasis,
CC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
CC asthma and bronchiectasis, intestinal disorders, spleen associated
CC diseases, modulate renal disorders, treat cardiovascular disorders such
CC as ischemic heart disease, modulate the proliferation, differentiation,
CC and/or function of bone and cartilage cells and to treat bone and/or
CC cartilage associated diseases or disorder. They may also be used to treat
CC disorders associated with the ovaries, cerebral oedema, hydrocephalus,
CC brain herniations, iatrogenic disease, inflammations, bacterial and viral
CC meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's
CC disease, multiple sclerosis, brain cancers, hydrocephalus and
CC encephalitis, and treat hepatic disorders
XX
XX Sequence 969 BP; 211 A; 316 C; 294 G; 148 T; 0 U; 0 Other;
SQ

Query Match 87.7%; Score 755.2; DB 3; Length 969;
Best Local Similarity 99.6%; Pred. No. 9e-146;
Matches 757; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 102 GGAGTACGGAGCTGGAGTTGTTGATCATCATCATCTGCTGGTGTGATGATGATGAT 161
Db 2 GGAGTACGGAGCTGGAGTTGTTGATCATCATCATCTGCTGGTGTGATGATGATGAT 61
Qy 162 GGTGGTGGTGTGATCAGCTGCTGAGCCACTACAGCTGTCTGACGGTCTTATCAG 221
Db 62 GGTGGTGGTGTGATCAGCTGCTGAGCCACTACAGCTGTCTGACGGTCTTATCAG 121
Qy 222 CCGGCACAGCCAGGGCGGAGAGATGCCCTGCTCTCAGAGGATGCTGTGGCC 281
Db 122 CCGGCACAGCCAGGGCGGAGAGATGCCCTGCTCTCAGAGGATGCTGTGGCC 181
Qy 282 CTGGAGAGCAGTGTCTAGGCAACGGAATCCAGAGCCGAGGTCTACGCCCGCTCG 341
Db 182 CTGGAGAGCAGTGTCTAGGCAACGGAATCCAGAGCCGAGGTCTACGCCCGCTCG 241
Qy 342 GCCACAGCAGCGCTGGCGTGGCGCTTCCGCCAGCGGGAGCGCTTCCACGGTCCA 401
Db 242 GCCACAGCAGCGCTGGCGTGGCGCTTCCGCCAGCGGGAGCGCTTCCACGGTCCA 301
Qy 402 GCCACCTATCCGTACTCTGAGCAGCAGATCCACCTCCACCCACCATCTCGTGTGAG 461
Db 302 GCCACCTATCCGTACTCTGAGCAGCAGATCCACCTCCACCCACCATCTCGTGTGAG 361
Qy 462 CGGGAGGAGCGCCCGACCCCTACAGGGCGCTGACCTTCAGCTTCGGGAGCCCGAGCA 521
Db 362 CGGGAGGAGCGCCCGACCCCTACAGGGCGCTGACCTTCAGCTTCGGGAGCCCGAGCA 421
Qy 522 GCAGCTGGAACTGAACCGGGAGTGGTGGCGGAGCGCCCGGAGGAGGAGTGGGCTG 581
Db 422 GCAGCTGGAACTGAACCGGGAGTGGTGGCGGAGCGCCCGGAGGAGGAGTGGGCTG 481
Qy 582 TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 641

PT New antibodies against tumor-associated antigenic target polypeptide,
PT useful for treating or diagnosing tumors or cancers in mammals, e.g.
PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
PT carcinomas.

PS Claim 2; Fig 44; 285pp; English.

CC ACC49493 to ACC49552 encode the human tumour-associated antigenic target
CC (TAT) proteins given in ABP97175 to ABP97234. The present invention
CC describes an isolated antibody that binds to a polypeptide having at
CC least 80 % sequence identity to any of the 60 150-800 residue amino acid
CC sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking
CC its associated signal peptide, encoded by any of the 60 2000-3000 base
CC pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have
CC cytostatic activity. The antibody can be used for treating or diagnosing
CC tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast
CC cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal
CC cell carcinomas, or thyroid cancer

SQ Sequence 1850 BP; 477 A; 472 C; 498 G; 403 T; 0 U; 0 Other;
Query Match 87.6%; Score 754.2; DB 7; Length 1850;
Best Local Similarity 98.3%; Pred. No. 1.6e-145;
Matches 762; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY	87	TTTGTTCAGAGCATGGAGATCAGGAGCTGAGTTTGTTCAGATCATCATCGTGT	146
DB	77	TCTCTCGCAACACGAGCATGCGGAGCTGAGTTTGTTCAGATCATCATCGTGT	136
QY	147	GGTGATGATGGTGTGATGGTGTGATCAGTGCCTGCTGAGCCACTCAAGCTGCTGC	206
DB	137	GGTGATGATGGTGTGATGGTGTGATCAGTGCCTGCTGAGCCACTCAAGCTGCTGC	196
QY	207	ACGGTCTTTCATCAGCGGCACAGCAGCGGGCGGAGAGAGATGCGCTTCTCTCAGA	266
DB	197	ACGGTCTTTCATCAGCGGCACAGCAGCGGGCGGAGAGAGATGCGCTTCTCTCAGA	256
QY	267	AGGATCCCTGTGCGCTCGGAGGACAGTGTGAGGACGGAATCCAGAGCCGACGT	326
DB	257	AGGATCCCTGTGCGCTCGGAGGACAGTGTGAGGACGGAATCCAGAGCCGACGT	316
QY	327	CTACGCGCGCTCGGCCACACGCGCTGCGCGCTGCGCGCTGCGCGCGGAGCG	386
DB	317	CTACGCGCGCTCGGCCACACGCGCTGCGCGCTGCGCGCTGCGCGCGGAGCG	376
QY	387	CTTCACCGCTTCAGCGCCACCTATCCGTACCTGACGACGAGATCGACTGCCACCC	446
DB	377	CTTCACCGCTTCAGCGCCACCTATCCGTACCTGACGACGAGATCGACTGCCACCC	436
QY	447	CATCTCGCTGTTCAGCGGGGAGAGCGCCACCTACACGCGCGCTGCGCGCTCG	506
DB	437	CATCTCGCTGTTCAGCGGGGAGAGCGCCACCTACACGCGCGCTGCGCGCTCG	496
QY	507	TCGGGACCGCGAGCAGTGGAATGAACTGAACTGCGGGAGTGTGCGGGACCCCG	566
DB	497	TCGGGACCGCGAGCAGTGGAATGAACTGAACTGCGGGAGTGTGCGGGACCCCG	556
QY	567	AACCATCTTCAGCAGTGACCTGATGATGATGCGAGGCTGGGCGGCGCTGCG	626
DB	557	AACCATCTTCAGCAGTGACCTGATGATGATGCGAGGCTGGGCGGCGCTGCG	616
QY	627	CAGTAATCGGGCATCAGCGCCACGTTGCTACGCGACGCGCGCGCATGAGAG	686
DB	617	CAGTAATCGGGCATCAGCGCCACGTTGCTACGCGACGCGCGCGCATGAGAG	676
QY	687	GCCACCTACAGCAGGTGATCGGCACCTACCGGGGCTCTCTTCCAGCAGCAG	746
DB	677	GCCACCTACAGCAGGTGATCGGCACCTACCGGGGCTCTCTTCCAGCAGCAG	736
QY	747	CAGTGGCGCGCTCTCTTGTGGAGGGGACCGGGCTCCACACACATCGCGCC	806
DB	737	CAGTGGCGCGCTCTCTTGTGGAGGGGACCGGGCTCCACACACATCGCGCC	796

QY 807 AGAGAGCGCAGCCATCTGGAGCAAGAGAGGATTAACAGAAAGGACACCTCTC 861
DB 797 AGAGAGCGCAGCCATCTGGAGCAAGAGAGGATTAACAGAAAGGACACCTCTC 851

RESULT 8

AAA75164
ID AAA75164 standard; cDNA; 969 BP.
XX
AC AAA75164;
XX
DT 15-JAN-2001 (first entry)
XX
XX cDNA clone encoding a human TANGO 261 polypeptide.
XX
XX TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
KW cellular proliferation; cellular differentiation; cellular adhesion;
KW von Willebrand factor-associated disorder; cell trafficking; cancer;
KW hematopoietic associated disease; atelectasis; pulmonary congestion;
KW oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
KW intestinal disorder; spleen associated disease; renal disorder;
KW cardiovascular disorder; ischemic heart disease; hydrocephalus;
KW brain herniation; iatrogenic disease; inflammation; meningitis;
KW Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
KW multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 6..764
FT
FT /*tag= a
FT /product= "TANGO 261"
XX
XX WO200052022-A1.
XX
XX 08-SEP-2000.
XX
XX 01-MAR-2000; 2000WO-US005226.
XX
XX 01-MAR-1999; 99US-0122458P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
XX
XX WPI; 2000-579269/54.
XX P-PSDB; AAB18462.
XX
XX Novel human and murine secreted proteins designated TANGO 216, 261, 262,
XX 266 and 267 useful as modulating agents of cellular processes, e.g. for
XX treating cancer.
XX
XX Disclosure; Page; 175pp; English.

XX AAA75163-65 encode human TANGO 261 proteins. The specification also
XX describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO
XX polypeptides can be used to modulate cellular proliferation, modulate
XX cellular differentiation and/or modulate cellular adhesion. The proteins
XX can be used to treat any von Willebrand factor-associated disorder,
XX regulate extracellular matrix structuring, cellular adhesion, and cell
XX trafficking and/or migration, modulate cellular interactions, modulate
XX cell adhesion in proliferative disorders, such as cancer, modulate the
XX proliferation, differentiation, and/or function of cells that appear in
XX the bone marrow, and leukocytes, treat bone marrow, blood and
XX hematopoietic associated diseases and disorders, atelectasis, pulmonary
XX congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and
XX bronchiectasis, intestinal disorders, spleen associated diseases,
XX modulate renal disorders, treat cardiovascular disorders such as ischemic
XX heart disease, modulate the proliferation, differentiation, and/or
XX function of bone and cartilage cells and to treat bone and/or cartilage
XX associated diseases or disorder. They may also be used to treat disorders
XX associated with the ovaries, and cerebral oedema, hydrocephalus, brain
XX herniations, iatrogenic disease, inflammations, bacterial and viral

Db 2 GGAGATGGCGGACCTGAGTTTGTTCAGATCATCATCGTGTGTATGATGAT 61
Qy 162 GTGGTGTGATCAGCTGCTGTGAGCCACTAACAAGCTGTGTGACGGTCTTTCATCAG 221
Db 62 GTGGTGTGATCAGCTGCTGTGAGCCACTAACAAGCTGTGTGACGGTCTTTCATCAG 121
Qy 222 CCGGCACAGCCAGGGCGGAGGAGAGATGCTGTCTCAGAGGATGCTGTGGCC 281
Db 122 CCGGCACAGCCAGGGCGGAGGAGAGATGCTGTCTCAGAGGATGCTGTGGCC 181
Qy 282 CTCGGAGAGACAGTGTTCAGGCAACGGAATCCAGAGCCGCGAGTCTACGCCCGCTCG 341
Db 182 CTCGGAGAGACAGTGTTCAGGCAACGGAATCCAGAGCCGCGAGTCTACGCCCGCTCG 241
Qy 342 GCCCACCAGCGCTGCGCTGCGGCTTTCGCGCCAGCGGAGGCTTCACCGCTTCCA 401
Db 242 GCCCACCAGCGCTGCGCTGCGGCTTTCGCGCCAGCGGAGGCTTCACCGCTTCCA 301
Qy 402 GCCCACCATTCCTGACGACGACGATGCGACCTGCGCACCCACCATCTTCGCTGTCAGA 461
Db 302 GCCCACCATTCCTGACGACGACGATGCGACCTGCGCGCCACCATCTTCGCTGTCAGA 361
Qy 462 CGGGAGAGCCCGCCACCTTACAGGCGCCCTGCACTTCCAGCTTGGGAGCCCGGAGCA 521
Db 362 CGGGAGAGCCCGCCACCTTACAGGCGCCCTGCACTTCCAGCTTGGGAGCCCGGAGCA 421
Qy 522 GCAGCTGGAATGTAACCGGAGTGGTGGCGGACCCCAACAGAACCATCTTCGACAG 581
Db 422 GCAGCTGGAATGTAACCGGAGTGGTGGCGGACCCCAACAGAACCATCTTCGACAG 481
Qy 582 TGACCTGATGATAGTGTCCAGGCTGGCGGCGCCCTGCGCCCGCCAGAGTAACCTCGGCGAT 641
Db 482 TGACCTGATGATAGTGTCCAGGCTGGCGGCGCCCTGCGCCCGCCAGAGTAACCTCGGCGAT 541
Qy 642 CAGCGCCAGCTGTACGCGGAGCGCGGCGCATGAGGGGCGCGCCGACCTACAGCGA 701
Db 542 CAGCGCCAGCTGTACGCGGAGCGCGGCGCATGAGGGGCGCGCCGACCTACAGCGA 601
Qy 702 GGTGATCGGCATACCGCGGCTCTCTTCAGCAGCAGCAGAGTGGCGCGCCCTC 761
Db 602 GGTGATCGGCATACCGCGGCTCTCTTCAGCAGCAGCAGAGTGGCGCGCCCTC 661
Qy 762 CTGCTGGAGGAGCGGCTCCACACACACATCGCGCCCTAGAGAGCGCGCCAT 821
Db 862 CTGCTGGAGGAGCGGCTCCACACACACATCGCGCCCTAGAGAGCGCGCCAT 721
Qy 822 CTGGAGCAAGAGAGGATTAACAGAAAGGACACCTCTC 861
Db 722 CTGGAGCAAGAGAGGATTAACAGAAAGGACACCTCTC 761

RESULT 10
ID AAA75165 standard; cDNA; 969 BP.
AC AAA75165;
XX
DT 15-JAN-2001 (first entry)
XX
DE cDNA clone encoding a human TANGO 261 polypeptide.
XX

TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
cellular proliferation; cellular differentiation; cellular adhesion;
von Willebrand factor-associated disorder; cell trafficking; cancer;
hematopoietic associated disease; atelectasis; pulmonary congestion;
edema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
intestinal disorder; spleen associated disease; renal disorder;
cardiovascular disorder; ischemic heart disease; hydrocephalus;
brain herniation; iatrogenic disease; inflammation; meningitis;
Alzheimer's disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.

OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 6..764
FT /**tag= a
FT /product= "TANGO 261"
XX
PN WC200052022-AL.
XX PD 08-SEP-2000.
XX
XX 01-MAR-2000; 2000WO-US005226.
XX PF
XX 01-MAR-1999; 99US-0122458P.
XX PR
XX (MILL-) MILLENNIUM PHARM INC.
XX PA
XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
XX PI
XX WPI; 2000-579269/54.
XX DR P-PSDB; AAB18463.
XX
XX Novel human and murine secreted proteins designated TANGO 216, 261, 262,
PT 266 and 267 useful as modulating agents of cellular processes, e.g. for
PT treating cancer.
XX
XX Disclosure; Page; 175pp; English.
XX
XX AAA75163-65 encode human TANGO 261 proteins. The specification also
CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO
CC polypeptides can be used to modulate cellular proliferation, modulate
CC cellular differentiation and/or modulate cellular adhesion. The proteins
CC can be used to treat any von Willebrand factor-associated disorder,
CC regulate extracellular matrix structuring, cellular adhesion, and cell
CC trafficking and/or migration, modulate cellular interactions, modulate the
CC cell adhesion in proliferative disorders, such as cancer, modulate the
CC proliferation, differentiation, and/or function of cells that appear in
CC the bone marrow, and leukocytes, treat bone marrow, blood and
CC hematopoietic associated diseases and disorders, atelectasis, pulmonary
CC congestion or edema, emphysema, chronic bronchitis, bronchial asthma and
CC bronchiectasis, intestinal disorders, spleen associated diseases,
CC moderate renal disorders, treat cardiovascular disorders such as ischemic
CC heart disease, modulate the proliferation, differentiation, and/or
CC function of bone and cartilage cells and to treat bone and/or cartilage
CC associated diseases or disorder. They may also be used to treat disorders
CC associated with the ovaries, and cerebral oedema, hydrocephalus, brain
CC herniations, iatrogenic disease, inflammations, bacterial and viral
CC meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's
CC disease, multiple sclerosis, brain cancers, hydrocephalus and
CC encephalitis, and treat hepatic disorders. note: the present sequence
CC does not appear in the specification; it was created using information
CC provided
XX
SQ Sequence 969 BP; 210 A; 317 C; 294 G; 148 T; 0 U; 0 Other;
Query Match 87.5%; Score 753.6; DB 3; Length 969;
Best Local Similarity 99.5%; Pred. No. 1.9e-145;
Matches 756; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 102 GGAGATCGGAGCTGGAGTTTGTTCAGATCATCATCGTGTGTATGATGATGAT 161
Db 2 GGAGATCGGAGCTGGAGTTTGTTCAGATCATCATCGTGTGTATGATGATGAT 61
Qy 162 GTGGTGTGATCAGCTGCTGTGAGCCACTAACAAGCTGTGTGACGGTCTTTCATCAG 221
Db 62 GTGGTGTGATCAGCTGCTGTGAGCCACTAACAAGCTGTGTGACGGTCTTTCATCAG 121
Qy 222 CCGGCACAGCCAGGGCGGAGGAGAGATGCTGTCTCAGAGGATGCTGTGGCC 281
Db 122 CCGGCACAGCCAGGGCGGAGGAGAGATGCTGTCTCAGAGGATGCTGTGGCC 181
Qy 282 CTCGGAGAGACAGTGTTCAGGCAACGGAATCCAGAGCCGCGAGTCTACGCCCGCTCG 341

Db 182 CTCGAGAGACAGTGTGAGGAAATCCAGAGCGCAGGTCTACGCCCGCGCTCG 241
Qy 342 GCCACACGACCGCTGGCGGCGCTTCCAGCGGAGCGCTTCCACGCGCTTCCA 401
Db 242 GCCACACGACCGCTGGCGGCGCTTCCAGCGGAGCGCTTCCACGCGCTTCCA 301
Qy 402 GCCACCTATCGTACTGTGACGACGAGATCGACTGCCACCCACCATCTCGTGTGAGA 461
Db 302 GCCACCTATCGTACTGTGACGACGAGATCGACTGCCACCCACCATCTCGTGTGAGA 361
Qy 462 CGGGAGAGAGCCCGACCTACCGGGCCCTGACCGCTCCAGCTTCGGGACCCCGAGCA 521
Db 362 CGGGAGAGAGCCCGACCTACCGGGCCCTGACCGCTCCAGCTTCGGGACCCCGAGCA 421
Qy 522 CGAGCTGGAATGAACCGGGAGTGGTGGCGCACCCCGCCAAACAGAACCATCTTCGACAG 581
Db 422 CGAGCTGGAATGAACCGGGAGTGGTGGCGCACCCCGCCAAACAGAACCATCTTCGACAG 481
Qy 582 TGACCTGATGATGATGACCGGCGGCGGCGCTTCCAGCGGAGCGCTTCCAGCGGAGCGAT 641
Db 482 TGACCTGATGATGATGACCGGCGGCGGCGCTTCCAGCGGAGCGCTTCCAGCGGAGCGAT 541
Qy 642 CAGCGCCACGTGTACGCGACGCGGCGGCGCATGAGAGGCGCGCGCCACCTACAGCGA 701
Db 542 CAGCGCCACGTGTACGCGACGCGGCGGCGCATGAGAGGCGCGCGCCACCTACAGCGA 601
Qy 702 GGTGATCGGCACCTACCGGGGTCTCTCTCCAGCACCGAGAGCGGCGCGCTC 761
Db 602 GGTGATCGGCACCTACCGGGGTCTCTCTCCAGCACCGAGAGCGGCGCGCTC 661
Qy 762 CTTGCTGAGGGGACCCGGCTCCACACACACATCGCGCGCCCTAGAGAGCGGAGCCAT 821
Db 662 CTTGCTGAGGGGACCCGGCTCCACACACACATCGCGCGCCCTAGAGAGCGGAGCCAT 721
Qy 822 CTGGAGCAAGAGAGGATTAACAGAAAGGACCCCTCTC 861
Db 722 CTGGAGCAAGAGAGGATTAACAGAAAGGACCCCTCTC 761

RESULT 11

ID AAD60105 standard; cDNA; 1140 BP.
AC AAD60105;
XX AAD60105;
XX AAD60105;
DT 18-DEC-2003 (first entry)
XX Human androgen-regulated gene (ARG), PMEPAL.
XX Human androgen-regulated gene (ARG), PMEPAL; prostate cancer;
KW Human; androgen-regulated gene; ARG; PMEPAL; prostate cancer;
KW chromosome 20q13; gene; ss.
XX Homo sapiens.
XX Homo sapiens.
PH Key Location/Qualifiers
FT 95..1853
CDS /*tag= a
FT /product= "Human PMEPAL protein"
FT /note= "CDS is referred to as SEQ ID NO:2 in claim 1 of
FT the specification"
XX
XX US566130-B1.
XX
XX 20-MAY-2003.
XX
XX 26-JAN-2001; 2001US-00769482.
XX
XX 28-JAN-2000; 2000US-0178772P.
PR 31-JAN-2000; 2000US-0179045P.
XX
XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
PA Srivastava S, Moul JW, Xu LL, Segawa T;
XX
PI

XX WPI; 2003-719644/68.
DR P-PSDB; AAE39589.
XX
PT Novel isolated androgen-regulated gene designated as PMEPAL useful for
FT selecting primers and probes for detecting prostate cancer cells in
FT biological samples by nucleic acid amplification techniques.
XX
XX Example 7; Col 29-30; 58pp; English.
XX
CC The invention relates to an isolated androgen-regulated gene (ARG)
CC designated as PMEPAL. The invention is useful for selecting primers and
CC probes for detecting prostate cancer cells in a biological sample by
CC using nucleic acid amplification techniques. The present sequence is
CC human PMEPAL cDNA. PMEPAL gene chromosome 20q13
XX
SQ Sequence 1140 BP; 271 A; 349 C; 336 G; 184 T; 0 U; 0 Other;
Query Match 87.5%; Score 753.6; DB 9; Length 1140;
Best Local Similarity 99.5%; Pred No. 2e-145;
Matches 756; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 102 GGAGATCACGAGCTGGAGTTTGTTCAGATCATCATCATCGTGTGTGTGATGATGAT 161
Db 91 GGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGTGTGTGATGATGAT 150
Qy 162 GGTGTGTGTATCAGTGCCTGCTGAGCCACTACAAGTGTCTGCACGTCCTTCATCAG 221
Db 151 GGTGTGTGTATCAGTGCCTGCTGAGCCACTACAAGTGTCTGCACGTCCTTCATCAG 210
Qy 222 CCGGCA CAGCCAGGCGCGGAGGAGAGATGCCCTGTCTCAGAAAGATGCTGTGGCC 281
Db 211 CCGGCA CAGCCAGGCGCGGAGGAGAGATGCCCTGTCTCAGAAAGATGCTGTGGCC 270
Qy 282 CTCGAGAGCACAGTGTGAGGCAACGGAATCCAGAGCGCAGGTCACGCCCGCTCG 341
Db 271 CTCGAGAGCACAGTGTGAGGCAACGGAATCCAGAGCGCAGGTCACGCCCGCTCG 330
Qy 342 GCCACCGACCGCTGGCGCTTCCAGCGGAGCGCTTCCACCGCTTCCA 401
Db 331 GCCACCGACCGCTGGCGCTTCCAGCGGAGCGCTTCCACCGCTTCCA 390
Qy 402 GCCACCTATCGTACTGTGAGGAGATGACCTGCCACCGCTTCCAGCGCTTCCA 461
Db 391 GCCACCTATCGTACTGTGAGGAGATGACCTGCCACCGCTTCCAGCGCTTCCA 450
Qy 462 CGGGAGGAGCGCCCGACCTTACAGAGCGCGCTTCCAGCGCTTCCAGCGCTTCCA 521
Db 451 CGGGAGGAGCGCCCGACCTTACAGAGCGCGCTTCCAGCGCTTCCAGCGCTTCCA 510
Qy 522 GCAGCTGGAATGAACCGGGAGTGGTGGCGCACCCCGCCAAACAGAACCATCTTCGACAG 581
Db 511 GCAGCTGGAATGAACCGGGAGTGGTGGCGCACCCCGCCAAACAGAACCATCTTCGACAG 570
Qy 582 TGACCTGATGATGATGACCGGCGGCGGCGCTTCCAGCGGAGCGCTTCCAGCGGAGCGAT 641
Db 571 TGACCTGATGATGATGACCGGCGGCGGCGCTTCCAGCGGAGCGCTTCCAGCGGAGCGAT 630
Qy 642 CAGCGCCACGTGTACGCGAGCGCGGCGCATGAGAGGCGCGCGCCACCTACAGCGGA 701
Db 631 CAGCGCCACGTGTACGCGAGCGCGGCGCATGAGAGGCGCGCGCCACCTACAGCGGA 690
Qy 702 GGTGATCGGCACCTACCGGGGTCTCTCTTCCAGCACCGAGAGCGAGTGGGCGCGCTC 761
Db 691 GGTGATCGGCACCTACCGGGGTCTCTCTTCCAGCACCGAGAGCGAGTGGGCGCGCTC 750
Qy 762 CTTGCTGAGGGGACCCGGCTCCACACACATCGCGCGCCCTAGAGAGCGGAGCCAT 821
Db 751 CTTGCTGAGGGGACCCGGCTCCACACACATCGCGCGCCCTAGAGAGCGGAGCCAT 810
Qy 822 CTGGAGCAAGAGAGGATTAACAGAAAGGACCCCTCTC 861
Db 811 CTGGAGCAAGAGAGGATTAACAGAAAGGACCCCTCTC 850

RESULT 12

ACC49537
 ID ACC49537 standard; cDNA; 806 BP.
 XX AC ACC49537;
 XX DT
 XX 01-JUL-2003 (first entry)
 DE Tumour-associated antigenic target protein TAR375 cDNA SEQ ID NO:45.
 XX KW Human; tumour-associated antigenic target; TAR; tumour; diagnosis;
 XX KW cancer; gene; ss.
 XX OS Homo sapiens.
 XX PN W02003024392-A2.
 XX PD 27-MAR-2003.
 XX PF 11-SEP-2002; 2002WO-US028859.
 XX PR 18-SEP-2001; 2001US-0323268P.
 XX PR 19-OCT-2001; 2001US-0339227P.
 XX PR 07-NOV-2001; 2001US-0336827P.
 XX PR 02-NOV-2001; 2001US-0331906P.
 XX PR 02-JAN-2002; 2002US-0345444P.
 XX PR 03-APR-2002; 2002US-0369724P.
 XX PR 19-AUG-2002; 2002US-0404809P.
 XX PA (GETH) GENENTECH INC.
 XX PI Frantz G, Hillan KJ, Phillips HS, Polakis P, Spencer SD;
 XX PI Williams PM, Wu TD, Zhang Z;
 XX DR WPI: 2003-354551/33.
 XX DR P-PSDB; ABP97219.
 XX PT New antibodies against tumor-associated antigenic target polypeptide,
 XX PT useful for treating or diagnosing tumors or cancers in mammals, e.g.
 XX PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
 XX PT carcinomas.
 XX PS Claim 2; Fig 45; 285pp; English.

ACC49493 to ACC49552 encode the human tumour-associated antigenic target
 (TAT) proteins given in ABP97175 to ABP97234. The present invention
 describes an isolated antibody that binds to a polypeptide having at
 least 80 % sequence identity to any of the 60 150-800 residue amino acid
 sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking
 its associated signal peptide, encoded by any of the 60 2000-3000 base
 pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have
 cytosolic activity. The antibody can be used for treating or diagnosing
 tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast
 cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal
 cell carcinomas, or thyroid cancer

Sequence 806 BP; 161 A; 286 C; 241 G; 118 T; 0 U; 0 Other;
 Query Match 87.4%; Score 752.6; DB 7; Length 806;
 Best Local Similarity 98.2%; Pred. No. 3e-145;
 Matches 761; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

87 TTTCCTCCAGCATGAGATCAGGAGCGGAGTTGTTCAGATCATCATCATCTGCTG 146
 14 TCTCCTCGGAACAGGCAATGCGGAGCTGGAGTTGTTCAGATCATCATCATCTG 73
 147 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 206
 74 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 133
 207 ACGTCTCTTCATACGCGCGGCACAGCCAGGCGGAGGAGAGATGCTCTCTCAGA 266

Db	134	ACGTCCTTCATAGCCGGCACACCCAGGGCGGAGAGAGATGCCCTTCTCTCAGA	193
Qy	267	AGGATGCTGTGGCCCTCGGAGAGCACAGTGTTCAGGCAACGGAAATCCAGAGCCGAGGT	326
Db	194	AGGATGCTGTGGCCCTCGGAGAGCACAGTGTTCAGGCAACGGAAATCCAGAGCCGAGGT	253
Qy	327	CTAGCCCGCGCTCGGCCACCGACCGCTGGCGTGGCGCTTCCGCGCCGCGGAGCG	386
Db	254	CTAGCCCGCGCTCGGCCACCGACCGCTGGCGTGGCGCTTCCGCGCCGCGGAGCG	313
Qy	387	CTTCCACCGCTTCCAGCCACCTATCGGTACCTGACGACGAGATCGACCTGCCACCCAC	446
Db	314	CTTCCACCGCTTCCAGCCACCTATCGGTACCTGACGACGAGATCGACCTGCCGCCCCAC	373
Qy	447	CATCTCGCTGTACAGCGGAGAGCCCCACCTTACAGGGCCCCCTGCACTTCCAGCT	506
Db	374	CATCTCGCTGTACAGCGGAGAGCCCCACCTTACAGGGCCCCCTGCACTTCCAGCT	433
Qy	507	TCGGGACCCCGAGCAGCAGTGGAACTGAACCGGGAGTCGGTGGCGGCACACCCCAACAG	566
Db	434	TCGGGACCCCGAGCAGCAGTGGAACTGAACCGGGAGTCGGTGGCGGCACACCCCAACAG	493
Qy	567	AACCATCTTCAGCAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG	626
Db	494	AACCATCTTCAGCAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATG	553
Qy	627	CAGTAACTTCGGGCGCATCAGCGCCACGCTGCTAGCGGCGGCGGCGGCGGCGGCGGCG	686
Db	554	CAGTAACTTCGGGCGCATCAGCGCCACGCTGCTAGCGGCGGCGGCGGCGGCGGCGGCG	613
Qy	687	GCCACCTTACAGCAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG	746
Db	614	GCCACCTTACAGCAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG	673
Qy	747	CAGTGGGCGCGCTTCCTGCTGGAGGAGCGCGCTCCACACACACACATCGGCGCCCT	806
Db	674	CAGTGGGCGCGCTTCCTGCTGGAGGAGCGCGCTCCACACACACACATCGGCGCCCT	733
Qy	807	AGAGAGCGCAGCCATCTGGAGCAAGAGAGGATAAAGAGAGAGAGAGAGAGAGAGAGAG	861
Db	734	AGAGAGCGCAGCCATCTGGAGCAAGAGAGGATAAAGAGAGAGAGAGAGAGAGAGAGAG	788

RESULT 13

AAA47429
 ID AAA47429 standard; DNA; 1061 BP.

XX AC AAA47429;

DT 20-OCT-2000 (first entry)

XX Sequence encoding human neuron-associated protein.

XX Neuron associated protein; NEUP; neurological disorder; epilepsy;
 XX ischemic cerebrovascular disease; stroke; cerebral neoplasm;
 XX Alzheimer's disease; Pick's disease; Huntington's disease; dementia;
 XX Parkinson's disease; demyelinating disease; meningitis; prion disease;
 XX kuru; Creutzfeldt-Jakob disease; neurofibromatosis; cerebral palsy;
 XX muscular dystrophy; central nervous system; CNS;
 XX peripheral nervous system; PNS; myopathy; schizophrenia;
 XX actinic keratosis; arteriosclerosis; atherosclerosis; bursitis;
 XX cirrhosis; hepatitis; mixed connective tissue disease; MCTD;
 XX myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer;
 XX autoimmune disease; inflammation; acquired immunodeficiency syndrome;
 XX AIDS; Addison's disease; adult respiratory distress syndrome; allergy;
 XX ankylosing spondylitis; amyloidosis; anaemia; asthma;
 XX Werner syndrome; trauma; human; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX CDS 101..859

FT /*tag= a
FT /product= "Neuron associated protein"
XX
PN
XX
XX
PD WO200034477-A2.
XX
XX 15-JUN-2000.
XX
XX 10-DEC-1999; 99WO-US030408.
XX
XX 11-DEC-1998; 98US-00210083.
PR 09-FEB-1999; 99US-0119365P.
PR 16-MAR-1999; 99US-0124687P.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Tang YT, Yue H, Baughn MR, Hillman JL, Lal P, Au-Young J;
PI Yang JY, Lu DAM, Azimzai Y;
XX
XX WPI: 2000-423423/36.
DR P-PSDB; AAB01398.
XX

XX New human neuron-associated proteins and polynucleotides encoding them,
XX useful for diagnosis, treatment and prevention of cell proliferative
XX disorders including cancer, neuronal and neurological disorders.
XX
XX Claim 9; Page 136; 145pp; English.

XX Human neuron-associated proteins (NEUPAP) can be used for for treating or
XX preventing a disorder associated with decreased expression or activity of
XX NEUPAP. Antagonists of NEUPAP are useful for treating or preventing
XX disorder associated with increased expression or activity of NEUPAP. NEUPAP
XX or their fragments or derivatives are useful for treating neurological
XX disorder such as epilepsy, ischemic cerebrovascular disease, stroke,
XX cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's
XX disease, dementia and Parkinson's disease. NEUPAPs are also useful for
XX treating other demyelinating diseases, bacterial and viral meningitis,
XX prion diseases including kuru, Creutzfeldt-Jakob disease, nutritional and
XX metabolic diseases of the nervous system, neurofibromatosis, other
XX developmental disorders of the central nervous system, cerebral palsy,
XX neuroskeletal disorders, autonomic nervous system disorders, cranial
XX nerve disorders, spinal cord diseases, muscular dystrophy and other
XX neuromuscular disorders, peripheral nervous system disorders, inherited,
XX metabolic, endocrine, and toxic myopathies, mental disorders including
XX mood, anxiety and schizophrenic disorders, a cell proliferative disorder
XX such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis,
XX cirrhosis, hepatitis, mixed connective tissue disease (MCTD),
XX myelofibrosis, paroxysmal nocturnal haemoglobinuria, cancers of the
XX adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, and an
XX autoimmune/inflammatory disorder such as acquired immunodeficiency
XX syndrome (AIDS), Addison's disease, adult respiratory distress syndrome,
XX allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, Werner
XX syndrome, complications of cancer, hemodialysis, and extracorporeal
XX circulation, viral, bacterial, fungal parasitic, protozoal, and
XX helminthic infections, and trauma. This sequence was given the Incyte ID
XX no. 1871288CB1

XX SQ Sequence 1061 BP; 225 A; 342 C; 326 G; 168 T; 0 U; 0 Other;

Query Match 87.4%; Score 752.6; DB 3; Length 1061;
Best Local Similarity 98.2%; Pred. NO. 3.1e-145;
Matches 761; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 87 TTGTTCAGAGATGAGATACCGAGCTGGAGTTGTTCAGATCATCATCATCGTGT 146
DB 82 TCCTCCGCGAACCAGCAATGCGGAGCTGGAGTTGTTCAGATCATCATCATCGTGT 141
QY 147 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 206
DB 142 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 201
QY 207 ACGGTCTTTCATCAGCCGACACCGAGGCGGAGGAGAGATGCGCTGCTCTCAGA 266
DB 202 ACGGTCTTTCATCAGCCGCGACACCGAGGCGGAGGAGAGATGCGCTGCTCTCAGA 261

QY 267 AGGATGCTGTGGCCCTCGAGAGACACAGTGTTCAGGCAACGGAATCCAGAGACCGCAGGT 326
DB 262 AGGATGCTGTGGCCCTCGAGAGACACAGTGTTCAGGCAACGGAATCCAGAGACCGCAGGT 321
QY 327 CTACGCGCGCTCGGCGCCACCGAGCGCTGGCGCTTTCGCGCCACGCGGAGCG 386
DB 322 CTACGCGCGCTCGGCGCCACCGAGCGCTGGCGCTTTCGCGCCACGCGGAGCG 381
QY 387 CTTTCCACCGCTTTCAGCGCCACCTATCCGTAACCTGAGACACGAGATCGACTGCCACCCAC 446
DB 382 CTTTCCACCGCTTTCAGCGCCACCTATCCGTAACCTGAGACACGAGATCGACTGCCACCCAC 441
QY 447 CATCTCGCTGTACAGCGGAGGAGCGCCACCGCTTTCAGGCGCGCTTTCAGCTCCAGCT 506
DB 442 CATCTCGCTGTACAGCGGAGGAGCGCCACCGCTTTCAGGCGCGCTTTCAGCTCCAGCT 501
QY 507 TCGGGAACCCCGAGCAGCAGCTGGAACCTGAACCGGAGTGGTGGCGGCAACCCCAACAG 566
DB 502 TCGGGAACCCCGAGCAGCAGCTGGAACCTGAACCGGAGTGGTGGCGGCAACCCCAACAG 561
QY 567 AACCATCTTCGACAGTACCTGATGATAGTTCAGGCTGGGCGCGCTTTCAGCTCCAGCT 626
DB 562 AACCATCTTCGACAGTACCTGATGATAGTTCAGGCTGGGCGCGCTTTCAGCTCCAGCT 621
QY 627 CAGTAACTCGGCGATCAGCGCCACCGCTTTCAGGCGCGCTTTCAGCTCCAGCTCCAGCT 686
DB 622 CAGTAACTCGGCGATCAGCGCCACCGCTTTCAGGCGCGCTTTCAGCTCCAGCTCCAGCT 681
QY 687 GCCCACTACAGCGAGTATCGGCACCTACCCGGGTCTCTTTCAGACACGACGAGAG 746
DB 682 GCCCACTACAGCGAGTATCGGCACCTACCCGGGTCTCTTTCAGACACGACGAGAG 741
QY 747 CAGTGGCGCGCTCTCTTGTGGAGGGGACCCGGCTTTCACACACACACATCGCGCCCT 806
DB 742 CAGTGGCGCGCTCTCTTGTGGAGGGGACCCGGCTTTCACACACACACATCGCGCCCT 801
QY 807 AGAGAGCGCAGCATCTCGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 861
DB 802 AGAGAGCGCAGCATCTCGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 856
RESULT 14
ADC37324
ID ADC37324 standard; DNA; 1085 BP.
XX
XX AC ADC37324;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DT Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 157.
XX
XX DE Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
XX cancer; infectious disease; bone disease; AIDS;
XX neurodegenerative disease; ischaemic disorder; Antiinflammatory;
XX Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-Hiv;
XX Neuroprotective; Nootropic; Cardiant; Gene therapy; human; gene; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO2003048202-A2.
XX
XX PD 12-JUN-2003.
XX
XX PF 03-DEC-2002; 2002WO-JP012644.
XX
XX PR 03-DEC-2001; 2001JP-00368692.
XX
XX PR 05-DEC-2001; 2001US-0335829P.
XX
XX PR 04-OCT-2002; 2002JP-00291302.
XX
XX PR 04-OCT-2002; 2002US-0415769P.
XX
XX PA (ASAH) ASAH KASEI KK.
XX

PI Matsuda A, Muramatsu S;
XX WPI: 2003-505282/47.
DR P-PSDB; ADC37325.
XX
PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
PT useful for treating inflammation, autoimmune diseases, cancers,
PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
PT ischemic disorders.
XX
PS Claim 4; SEQ ID NO 157; 938pp; English.
XX
CC The present invention relates to novel proteins and their coding
CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
CC kappaB). The proteins and their coding sequences are useful for treating
CC a disease associated with NF-kappaB activation, such as inflammation,
CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
CC neurodegenerative diseases, or ischaemic disorders.
XX
SQ Sequence 1085 BP; 223 A; 352 C; 334 G; 176 T; 0 U; 0 Other;

Query Match 87.4%; Score 752.6; DB 9; Length 1085;
Best Local Similarity 98.2%; Freq. NO. 3.1e-145;
Matches 761; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 87 TTGTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTGTTTCAGATCATCATCATCGTGT 146
Db 109 TCTCTCGGAACACGGAATGCGGAGCTGGAGTTGTTTCAGATCATCATCATCGTGT 168

QY 147 GGTGATGATGGTATGGTGTGTGATCAGTGCTGCTGAGCCACTCAAGCTGTCTGC 206
Db 169 GGTGATGATGGTATGGTGTGTGATCAGTGCTGCTGAGCCACTCAAGCTGTCTGC 228

QY 207 ACGGTCTCTTCATCAGCGCGGCACAGCAGCGGGCGGAGAGAGATGCTCTCTCAGA 266
Db 229 ACGGTCTCTTCATCAGCGCGGCACAGCAGCGGGCGGAGAGAGATGCTCTCTCAGA 288

QY 267 AGGATGCTGTGCTCTCGGAGAGCAAGTGTGAGCAACGGAATCCAGAGCGCGAGGT 326
Db 289 AGGATGCTGTGCTCTCGGAGAGCAAGTGTGAGCAACGGAATCCAGAGCGCGAGGT 348

QY 327 CTACGCGCCGCTCGCGCCACACCGCTGCGCGCGCGCCCTCGCGCCAGCGGAGCG 386
Db 349 CTACGCGCCGCTCGCGCCACACCGCTGCGCGCGCGCCCTCGCGCCAGCGGAGCG 408

QY 387 CTTTCCACCGCTTCAGCGCCACCTATCCGTACCTGACGACGAGATCGACTGCCACCCAC 446
Db 409 CTTTCCACCGCTTCAGCGCCACCTATCCGTACCTGACGACGAGATCGACTGCCACCCAC 468

QY 447 CATCTCGCTGTCAGCGGGAGAGCCGCCACCTACAGGGCCCTGACCCCTCCAGCT 506
Db 469 CATCTCGCTGTCAGCGGGAGAGCCGCCACCTACAGGGCCCTGACCCCTCCAGCT 528

QY 507 TCGGGACCCCGAGCAGCTGGAACCTGAACCGGGAGTGGTGGCGGCACCCGCCAACACAG 566
Db 529 TCGGGACCCCGAGCAGCTGGAACCTGAACCGGGAGTGGTGGCGGCACCCGCCAACACAG 588

QY 567 AACCATCTTCAGAGTGAACCTGATGATGTCAGAGCTGGGGCCCTGCCCCCCCCAG 626
Db 589 AACCATCTTCAGAGTGAACCTGATGATGTCAGAGCTGGGGCCCTGCCCCCCCCAG 648

QY 627 CAGTAACCTCGGGCATCAGCGCCACGTGCTACCGGCGGGCGGCGATGGAGGGGCGCGC 686
Db 649 CAGTAACCTCGGGCATCAGCGCCACGTGCTACCGGCGGGCGGCGATGGAGGGGCGCGC 708

QY 687 GCCACCTACAGGAGGTGATCGGCGCATACCGGGGGTCTCTTTCAGACACAGCAGAG 746
Db 709 GCCACCTACAGGAGGTGATCGGCGCATACCGGGGGTCTCTTTCAGACACAGCAGAG 768

QY 747 CAGTGGGCGCCCTCTCTTGTGGAGGGGACCCGGCTCCACACACACATCGCGCCCT 806
Db 769 CAGTGGGCGCCCTCTCTTGTGGAGGGGACCCGGCTCCACACACACATCGCGCCCT 828

QY 807 AGAGAGCGCGCCATCTGGAGCAAGAGAGGATATAACAGAAAGGACACCTCTC 861
Db 829 AGAGAGCGCGCCATCTGGAGCAAGAGAGGATATAACAGAAAGGACACCTCTC 883

RESULT 15
ABZ36103
ID ABZ36103 standard; cDNA; 1334 BP.
XX
AC ABZ36103;
XX
DT 10-FEB-2003 (first entry)
XX
DE Human secretory polynucleotide SPTM SEQ ID NO 267.
XX
KW Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;
KW asthma; Crohn's disease; neurological disorder; epilepsy; cancer;
KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
KW multiple sclerosis; Parkinson's disease; cell proliferative disorder;
KW anti-inflammatory; immunosuppressive; neuroprotective; nootropic;
KW neuroleptic; anticonvulsant; cyrostatic; antiparkinsonian; anxiolytic;
KW antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus;
KW secretory polynucleotide; secretory protein; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200283876-A2.
XX
PD 24-OCT-2002.
XX
PF 27-MAR-2002; 2002WO-US009921.
XX
PR 29-MAR-2001; 2001US-0280067P.
PR 29-MAR-2001; 2001US-0280068P.
PR 16-MAY-2001; 2001US-0291280P.
PR 17-MAY-2001; 2001US-0291829P.
PR 17-MAY-2001; 2001US-0291849P.
PR 19-JUN-2001; 2001US-0299428P.
PR 20-JUN-2001; 2001US-0299776P.
XX (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;
PI Daugherty SC, Dam TC, Liu TP, Nguyen DA, Kleefeld Y, Gerstein EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RV, Urashka ME;
XX
DR WPI: 2003-075543/07.
DR P-PSDB; ABP75660.
XX
PT New human secretory proteins and polynucleotides, useful for diagnosing,
PT treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),
PT neurological disorders (e.g. Alzheimer's), or cell proliferations or
PT cancers.
XX
PS Claim 1; SEQ ID NO 267; 458pp + Sequence Listing; English.
XX
CC The invention relates to a secretory polynucleotide (designated sptm)
CC comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a
CC naturally occurring polynucleotide sequence at least 90 % identical to
CC the polynucleotide sequence, a polynucleotide complementary to them or an
CC RNA equivalent of them. The polypeptide or polynucleotide are useful for
CC treating, preventing or diagnosing a disease or condition associated with
CC the expression of functional SPTM. These are particularly useful for
CC the diagnosis, treating or preventing autoimmune/inflammatory disorders
CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's
CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,
CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,
CC schizophrenia or amnesia), or cell proliferative disorders (e.g.
CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,

CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,
CC breast, cervix or prostate). Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 1334 BP; 299 A; 381 C; 394 G; 260 T; 0 U; 0 Other;

Query Match 87.4%; Score 752.6; DB 7; Length 1334;
Best Local Similarity 98.2%; Pred. No. 3.2e-145;
Matches 761; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 87 TTGTTCAGAGCATGGAGATCAGCGAGCTGGAGTTGTTTCAGATCATCATCATCGTGGT 146
Db 82 TCTCTGCGAACACGAGCAATGGCGAGCTGGAGTTGTTTCAGATCATCATCATCGTGGT 141

QY 147 GGTGATGATGGTATGGTGGTGGTATCACTGCTGCTGAGCCACTACAAGCTGTCTGC 206
Db 142 GGTGATGATGGTATGGTGGTGGTATCACTGCTGCTGAGCCACTACAAGCTGTCTGC 201

QY 207 AGGTCCTTTCATCAGCCGGCAGCAGCGGGGAGGAGAGAAGATGCCCTGTCTCAGA 266
Db 202 AGGTCCTTTCATCAGCCGGCAGCAGCGGGGAGGAGAGAAGATGCCCTGTCTCAGA 261

QY 267 AGGATGCTGTGGCCCTCGAGAGCACAGTGTACGGCAACGGAATCCAGAGCCGCGAGT 326
Db 262 AGGATGCTGTGGCCCTCGAGAGCACAGTGTACGGCAACGGAATCCAGAGCCGCGAGT 321

QY 327 CTACGCCCGCTCGGCCACCGACCGCTGCGTGGCGCCCTTCGCCAGCGGGAGCG 386
Db 322 CTACGCCCGCTCGGCCACCGACCGCTGCGTGGCGCCCTTCGCCAGCGGGAGCG 381

QY 387 CTTCCACCGCTTCCAGCCACCTATCCGTACCTGACGACGAGATCGACCTGCCACCCAC 446
Db 382 CTTCCACCGCTTCCAGCCACCTATCCGTACCTGACGACGAGATCGACCTGCCACCCAC 441

QY 447 CATCTCGTGTGACAGGGGAGAGCCGCCCTACAGGGCCCTTCGACCTCCAGCT 506
Db 442 CATCTCGTGTGACAGGGGAGAGCCGCCCTACAGGGCCCTTCGACCTCCAGCT 501

QY 507 TCGGAGCCCGAGCAGCTGGAATGAACCGGAGTCTGGTGGCGCACCCCAACAG 566
Db 502 TCGGAGCCCGAGCAGCTGGAATGAACCGGAGTCTGGTGGCGCACCCCAACAG 561

QY 567 AACCATCTTCGACAGTACCTGATGGATAGTCCAGGCTGGCGGCCCTTCGCCCCAG 626
Db 562 AACCATCTTCGACAGTACCTGATGGATAGTCCAGGCTGGCGGCCCTTCGCCCCAG 621

QY 627 CAGTAACTCGGCGATCAGCGCCACCTGCTACGGCAGCGCGCGCATGGAGGGCGGCC 686
Db 622 CAGTAACTCGGCGATCAGCGCCACCTGCTACGGCAGCGCGCGCATGGAGGGCGGCC 681

QY 687 GCCCACTACAGCAGGTCATCGGCCACTACCGGGGTCCTCTTCAGCACCAGCAGAG 746
Db 682 GCCCACTACAGCAGGTCATCGGCCACTACCGGGGTCCTCTTCAGCACCAGCAGAG 741

QY 747 CAGTGGGCGCCCTCTCTGCGAGGGACCGCGCTCCACACACACATCGGCCCT 806
Db 742 CAGTGGGCGCCCTCTCTGCGAGGGACCGCGCTCCACACACACATCGGCCCT 801

QY 807 AGAGCGCAGCCATCTGGAGCAAGAGAGGATAAAGAGAAAGACCCCTTC 861
Db 802 AGAGCGCAGCCATCTGGAGCAAGAGAGGATAAAGAGAAAGACCCCTTC 856

Search completed: May 12, 2004, 00:56:47
Job time : 395.646 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2004, 00:10:42 ; Search time 2585.37 Seconds
(without alignments)
9944.945 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861

Sequence: 1 atgcaccgcttgatgggggt.....aacagaaaggacaccccttc 861

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: em_estba.*
- 2: em_esthum.*
- 3: em_estlin.*
- 4: em_estmu.*
- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_htc.*
- 9: gb_est1.*
- 10: gb_est2.*
- 11: gb_htc.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estcom.*
- 17: em_gss_hum.*
- 18: em_gss_inv.*
- 19: em_gss_pin.*
- 20: em_gss_vit.*
- 21: em_gss_fun.*
- 22: em_gss_mam.*
- 23: em_gss_mus.*
- 24: em_gss_pro.*
- 25: em_gss_rod.*
- 26: em_gss_phg.*
- 27: em_gss_vrl.*
- 28: gb_gss1.*
- 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	811.8	94.3	1009	9	AL578575
c 2	807.6	93.8	1201	9	AL517150
c 3	743.6	86.4	967	13	BQ641849
c 4	700	81.3	1046	12	BM922276

RESULT 1
AL578575/c
LOCUS
DEFINITION
AL578575 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DK001VC24 3-PRIME, mRNA sequence.
ACCESSION
AL578575
VERSION
AL578575.2 GI:31316780
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1009)
Li W.B., Gruber C., Jessee J., and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12942781.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9945.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DK001BB12NP1&cluster=9945.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :

ALIGNMENTS

5	687.8	79.9	945	13	BU539219
6	687	79.8	951	9	AL558881
c 7	667.4	77.5	916	13	BQ954555
8	667.4	77.5	1007	9	AL558882
c 9	667	77.5	874	13	BX362396
10	662.8	77.0	850	13	BU602918
11	648	75.3	780	29	AY419334
12	614.6	71.4	1079	11	BC023092
13	607.4	70.5	609	13	BQ63742
14	603.6	70.1	1207	11	AK008976
15	578.4	67.2	890	13	BQ690750
16	570.4	66.2	973	13	BU169156
17	568.8	66.1	572	13	BX641317
c 18	568.2	66.0	782	12	BQ015170
19	550	63.9	551	12	BM141979
20	529.8	61.5	894	12	BI851941
c 21	519.4	60.3	729	13	BQ575741
c 22	518.8	60.0	730	12	BM677602
c 23	515.2	59.8	728	13	BU683523
24	504	58.5	780	29	AY419335
25	501.6	58.3	588	12	BM483503
26	487.8	56.7	1201	9	AL543170
27	487.6	56.6	646	29	CG784226
28	475.2	55.2	624	29	AY419336
29	468	54.4	857	12	BQ323347
c 30	465.8	54.1	744	13	BU414421
31	461	53.5	763	12	BI646175
c 32	445.6	51.8	693	9	AI761441
33	445.4	51.7	655	13	BQ691705
34	445.4	51.7	1280	13	BQ691500
35	443.6	51.5	651	14	CB554226
36	440	51.1	899	13	BU136912
37	432.8	50.3	964	13	BU859860
38	430	49.9	841	12	BI156703
39	429.6	49.9	646	13	BU859841
40	428.8	49.8	974	10	BB624904
41	428.2	49.7	655	12	BI853324
42	416.2	48.3	587	12	BI083462
43	411.6	47.8	1127	13	BU174654
44	411	47.7	582	10	BE553323
c 45	407.4	47.3	629	13	BU730650

BU539219 AGENCOURT
AL558881 AL558881
BQ954555 AGENCOURT
AL558882 AL558882
BX362396 BX362396
BU602918 AGENCOURT
AY419334 Homo sapi
BC023092 Mus muscu
BQ63742 hdl3h06.Y
AK008976 Mus muscu
BQ690750 AGENCOURT
BU169156 AGENCOURT
BX641317 DXF2P686K
BQ015170 UI-H-BD1-
BM141979 if25a11.Y
BI851941 603379004
BQ575741 UI-H-EZ1-
BM677602 UI-E-EOL-
BU683523 UI-CF-EC1
AY419335 Pan trogl
BM483503 536869 MA
AL543170 AL543170
CG784226 FHCRG-GT-
AY419336 Mus muscu
BQ323347 602421734
BU414421 603670223
BI646175 603276395
AI761441 wg65f07.x
BQ691705 AGENCOURT
BQ691500 AGENCOURT
CB554226 WMSP0052
BU136912 AGENCOURT
BU859860 AGENCOURT
BI156703 602922119
BU859841 AGENCOURT
BB624904 BB624904
BI853324 603379903
BI083462 602875788
BU174654 AGENCOURT
BE553323 ur44h02.Y
BU730650 UI-E-C11-

QY	301	GGCAACGGAAATCCAGAGCGGAGCTCTACGCCCGCGCTCGGCCCCAGCCAGCCGCTGGCC	360
Db	367	GGCAACGGAAATCCAGAGCGGAGCTCTACGCCCGCGCTCGGCCCCAGCCAGCCGCTGGCC	426
QY	361	GTGCCCGCCCTTCGCCCGAGCGGAGCGCTTCCACCGCTTCCAGCCACCACTATCCGTACCTG	420
Db	427	GTGCCCGCCCTTCGCCCGAGCGGAGCGCTTCCACCGCTTCCAGCCACCACTATCCGTACCTG	486
QY	421	CAGCAGAGATGACCTGCACTCCACCCATCTCGCTGTGAGAGCGGAGGAGGCCACCC	480
Db	487	CAGCAGAGATGACCTGCGCCGCCACCACTCTCGCTGTGAGAGCGGAGGAGGCCACCC	546
QY	481	TACCAAGGCGCCCTTCAGCAGCTTCCAGCTTCCGAGCCCGGAGCGAGCAGCTGGAATGAACTG	540
Db	547	TACCAAGGCGCCCTTCAGCAGCTTCCGAGCTTCCGAGCCCGGAGCGAGCAGCTGGAATGAACTG	606
QY	541	GAGTCGTGGCGGCGACCCCAACAGCAACCACTCTTCGACAGTGAAGTGAATGATGTC	600
Db	607	GAGTCGTGGCGGCGACCCCAACAGCAACCACTCTTCGACAGTGAAGTGAATGATGTC	666
QY	601	AGGCTGGGCGGCGCCCTTCGCGCCCGCCAGCAGTAACTCGGGCATCAGCGCCACGCTGCTACGCG	660
Db	667	AGGCTGGGCGGCGCCCTTCGCGCCCGCCAGCAGTAACTCGGGCATCAGCGCCACGCTGCTACGCG	726
QY	661	AGCGGCGG-GCGCATGAGAGGCGCGCGG-CGACCTACAGCGAGTATCGGCCACTA--	716
Db	727	AGCGGCGGCGCGCATGAGAGGCGCGCGG-CGACCTACAGCGAGTATCGGCCACTA--	786
QY	717	CCCGGGGTCTCTCTTCAGCAGCAGCAGTGGCGCGCCCTCTCTCTGCTGAGAGGGGAC	776
Db	787	CCCGGGGTCTCTCTTCAGCAGCAGCAGTGGCGCGCCCTCTCTCTGCTGAGAGGGGAC	846
QY	777	CCCGGGTCC 784	
Db	847	GGGGAACC 854	
RESULT 5			
LOCUS	BU539219	945 bp	mRNA
DEFINITION	AGENCOURT_10215265 NIH_MGC_107 Homo sapiens CDNA clone		
ACCESSION	IMAGE:6569922 5', mRNA sequence.		
VERSION	BU539219		
KEYWORDS	EST.		
SOURCE	BU539219.1 GI:22849660		
ORGANISM	Homo sapiens (human)		
REFERENCE	1 (bases 1 to 945)		
AUTHORS	NH-MGC http://mgi.nci.nih.gov/		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) DNA Distribution by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LICM2757 row: p column: 18 High quality sequence stop: 663.		
FEATURES	Location/Qualifiers		
source	1..945		
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	/clone="IMAGE:6569922"		
	/lab_host="DH10B (phage-resistant)"		
	/clone_lib="NIH_MGC_107"		

/note="Organ: breast; Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

Note: this is a NIM_MGC Library.

ORIGIN

Query Match 79.8%; Score 687.8; DB 13; Length 945;
 Best Local Similarity 96.6%; Pred. No. 1.3e-116;
 Matches 734; Conservative 0; Mismatches 23; Indels 3; Gaps 3;

QY	87	TTTGTTCAGACATCGAGATCACGAGCTGGAGTTTGTTCAGATCATCATCGTGGT	146
DB	65	TCTCCTCGGAACCAGGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCGTGGT	124
QY	147	GCTGATGATGATGCTGGTGGTGTATCATCGTCTGTGAGCCACTCAAGCTGTCTGC	206
DB	125	GCTGATGATGATGCTGGTGGTGTATCATCGTCTGTGAGCCACTCAAGCTGTCTGC	184
QY	207	ACGGTCCCTTCATCAGCCGACAGCCAGGCGGAGGAGAGATGCTCTCTCAG	266
DB	185	ACGGTCCCTTCATCAGTGGCAGCAGCGGCGGAGGAGAGATGCTCTCTCAG	244
QY	267	AGGATGCTGTGGCCCTCGAGAGCACATGCTCAGCAACCGAATCCAGAGCCCGAGT	326
DB	245	AGGATGCTGTGGCCCTCGAGAGCACATGCTCAGCAACCGAATCCAGAGCCCGAGT	304
QY	327	CTACGCCCGCTCGGCCACCGACCGCTGGCGGCTGGCGGCGGCTTCGCCAGCGGAGCG	386
DB	305	CTACGCCCGCTCGGCCACCGACCGCTGGCGGCGGCTTCGCCAGCGGAGCG	364
QY	387	CTTCCACCGCTTCCAGCCCACTATCCGTACCTGAGCAGCAGATCGACCCAC	446
DB	365	CTTCCACCGCTTCCAGCCCACTATCCGTACCTGAGCAGCAGATCGACCCAC	424
QY	447	CATCTCGCTGTGACAGCGGAGGAGCCCACTTACCAGGCGGCTTCGACCTCCAGT	506
DB	425	CATCTCGCTGTGACAGCGGAGGAGCCCACTTACCAGGCGGCTTCGACCTCCAGT	484
QY	507	TCGGACCCCGAGCAGCTGGAACTGAAACCGGAGTCTGGTGGCGCACCCCAACAG	566
DB	485	TCGGACCCCGAGCAGCTGGAACTGAAACCGGAGTCTGGTGGCGCACCCCAACAG	544
QY	567	AACCATCTTCGACAGTACCTGATGATGATGCTCAGGCTGGGCGGCGCTTCGCCCGCAG	626
DB	545	AACCATCTTCGACAGTACCTGATGATGATGCTCAGGCTGGGCGGCGCTTCGCCCGCAG	604
QY	627	CAGTAACCTCGGCACTCAGCGCCACCTGTCTACGCGAGCGGCGCATGGAGGCGCGCC	686
DB	605	CAGTAACCTCGGCACTCAGCGCCACCTGTCTACGCGAGCGGCGCATGGAGGCGCGCC	664
QY	687	GCCCACTTACAGCGAGTCTCGGCCACTACCGGGGTCTCTTTCAGCAACGACGAG	746
DB	665	GCCCACTTACAGCGAGTCTCGGCCACTACCGGGGTCTCTTTCAGCAACGACGAG	724
QY	747	CAGTGGGCGGCGCTTCTTGTGAGGGGACCCGCTCCACACACACATCGCG-CCC	804
DB	725	CAGTGGGCGGCGCTTCTTGTGAGGGGACCCGCTCCACACACACATCGTGC	784
QY	805	CTAGAGAGCGCAG-CCATCTGGAGCAAGAGAGATATAA	843
DB	785	CTAAGAGCGCAGCCCATCTGGAGCAAGAGAGATATAA	824

RESULT 6
AL558881/c
LOCUS
DEFINITION
Homo sapiens cDNA clone CS0DJ015YF12 3-PRIME, mRNA sequence.
AL558881
AL558881
951 bp
mRNA
linear
EST 31-MAY-2003
Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
AL558881

VERSION	AL558881.2	GI:31283014
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 951)	
TITLE	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.	
JOURNAL	Full-length cDNA libraries and normalization	
COMMENT	Unpublished (2001) On Feb 15, 2001 this sequence version replaced gi:12903836. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr was normalized. Library was constructed by Life Technologies, a division of invitrogen. This sequence belongs to sequence cluster 9945.r for more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DJ015DC06NP1&cluster=9945.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DJ015DC06NP1. Location/Qualifiers 1..951 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DJ015YF12" /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED" /cell_line="JURKAT" /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED" /notes="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	
FEATURES		
source		
ORIGIN		
Query Match	79.8%;	Score 687; DB 9; Length 951;
Best Local Similarity	99.0%;	Pred. No. 1.8e-116;
Matches	690; Conservative	1; Mismatches 6; Indels 0; Gaps 0;
QY	165	GGTGGTGAACAGTGTCTCTGAGCCACATACAAGCTGTCTGCACGGTCTTCATCAGCG 284
DB	854	GGATGTGWTCACTGCTCTGAGCACTACAAGGTGTCTGCACGGTCTTCATCAGCG 795
QY	225	GCACAGCCAGGGCGGAGAGAGATGCCCTGTCTCACAAGATGCTGTGGCCCTC 284
DB	794	GAACAGCCAGGGCGGAGAGAGATGCCCTGTCTCAGAAGATGCTGTGGCCCTC 735
QY	285	GGAGAGCACAGTGTCAAGCAACGGAAATCCAGAGCCGAGGTCTACGCCCGCTCGGCC 344
DB	734	GGAGAGCACAGTGTCAAGCAACGGAAATCCAGAGCCGAGGTCTACGCCCGCTCGGCC 675
QY	345	CACCGACCGCTGGCCGCTGCCCTTGGCCAGGGAGCGCTTCACACCGCTTCAGACC 404
DB	674	CACCGACCGCTGGCCGCTGCCCTTGGCCAGGGAGCGCTTCACACCGCTTCAGACC 615
QY	405	CACCTATTCGTACTCTGACGACAGAGATCGAATCTGCGACACCACTCTCGTGTGTCAGACGG 464
DB	614	CACCTATTCGTACTCTGACGACAGAGATCGAATCTGCGGCCCACTTCTCGTTTTAGACGG 555
QY	465	GGAGGAGCCCCCACTTACAGGGCCCTTGACACCTCTCGGACCCCGAGCAGCA 524
DB	554	GGAGGAGCCCCCACTTACAGGGCCCTTGACACCTCTCGGACCCCGAGCAGCA 495
QY	525	GCTGGAACCTGAACCGGGAGTCTGGTGGCGCACCCGCCAAACAGAACCACTCTTCGACAGTGA 584
DB	494	GCTGGAACCTGAACCGGGAGTCTGGTGGCGCACCCGCCAAACAGAACCACTCTTCGACAGTGA 435
QY	585	CCTGATGGATAGTGCAGGCTGGGCGGCCCTCTGCCGCCCGCCAGCAGTAACCTCGGCGATCAG 644

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9945.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DJ015DC06Q1&cluster=9945.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DJ015DC06Q1.
Location/Qualifiers
1. 1007
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10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source
1. 1007
Query Match 77.5%; Score 667.4; DB 9; Length 1007;
Best Local Similarity 99.0%; Pred. No. 7.6e-113;
Matches 690; Conservative 2; Mismatches 3; Indels 2; Gaps 2;

ORIGIN
165 GGTGGTATACGTCGCTGAGCCACTACAGCTGTCTGCAGCTCCTTCATCAGCG 224
Db 62 GGATGTATACGTCGCTGAGCCACTACAGCTGTCTGCAGCTCCTTCATCAGCG 121
Qy 225 GCACAGCGCGGCGGAGAGAGATGCCCTGTCTCAGAGAGATGCCCTGTGGCCCTC 284
Db 122 GCACAGCGCGGCGGAGAGAGATGCCCTGTCTCAGAGAGATGCCCTGTGGCCCTC 181
Qy 285 GGAGAGACAGTGTACAGCAACGAATCCAGAGCGCGAGTCTACGCCGCTCGGCC 344
Db 182 GGAGAGACAGTGTACAGCAACGAATCCAGAGCGCGCA-GTCTACGCCGCTCGGCC 240
Qy 345 CACGACCGCTGCGCTGCGCCCTTGGCCAGCGGAGCGCTTCCACCGCTTCAGCC 404
Db 241 CACGACCGCTGCGCTGCGCCCTTGGCCAGCGGAGCGCTTCCACCGCTTCAGCC 300
Qy 405 CACTATCGTACCTGAGCAGAGATGACCTGCGCCACCGACCATCTGCTGTCAGCG 464
Db 301 CACTATCGTACCTGAGCAGAGATGACCTGCGCCACCGACCATCTGCTGTCAGCG 360
Qy 465 GGAGAGCGCCACCTACAGAGCGCCCTGACCCCTCCAGCTCGGAGCCCGAGCAGCA 524
Db 361 GGAGAGCGCCACCTACAGAGCGCCCTGACCCCTCCAGCTCGGAGCCCGAGCAGCA 420
Qy 525 GCTGGAATGAACCGGAGTGGTGGCGGCAACCCCAACAGAACCATCTTCAGCAGTGA 584
Db 421 GCTGGAATGAACCGGAGTGGTGGCGGCAACCCCAACAGAACCATCTTCAGCAGTGA 480
Qy 585 CCTGATGATGATGCGAGGCTGGGCGGCGCTGCGCCCGCCAGCGATTAATCTGGGCTCAG 644
Db 481 CCTGATGATGATGCGAGGCTGGGCGGCGCTGCGCCCGCCAGCGATTAATCTGGGCTCAG 540
Qy 645 CGCCACGTGTACCGGAGCGCGCGCGATGGAGGGGCGCGCCCACTACAGCGAGGT 704
Db 541 CGCCACGTGTACCGGAGCGCGCGCGATGGAGGGGCGCGCCCACTACAGCGAGGT 600
Qy 705 CATGGCCACTACCGGGGCTCTCTTCAGCAGCAGCAGAGCGAGTGGGCGGCTCTT 764
Db 601 CATGGCCACTACCGGGGCTCTCTTCAGCAGCAGCAGAGCGAGTGGGCGGCTCTT 660
Qy 765 GCTGAGGGGACCGGGCTCCACACACACATCGCGCCCTTAGAGCGCGAGCCATCTG 824
Db 661 GCTGAGGGGACCGGGCTCCACACACACATCGCGCCCTTAGAGCGCGCA-SCATCTG 719

Qy 825 GAGCAAGAGAGGATTAACAGAGAGGACACCCCTCTC 861
Db 720 GAGCAAGAGAGGATTAACAGAGAGGACACCCCTCTC 756

RESULT 9
BX362396/c
LOCUS BX362396
DEFINITION Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cDNA clone CS0DJ014IN15 3-PRIME, mRNA sequence.
ACCESSION BX362396
VERSION BX362396
KEYWORDS BX362396.1 GI:30378625
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 874)
AUTHORS Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9945.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DJ014CG08NP1&cluster=9945.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DJ014CG08NP1.
Location/Qualifiers
1. 874
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ014IN15"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 77.5%; Score 667; DB 13; Length 874;
Best Local Similarity 95.9%; Pred. No. 8.7e-113;
Matches 693; Conservative 16; Mismatches 11; Indels 2; Gaps 2;

Qy 151 ATGATGGTATGGTGGTGGTATC-ACGTGGCTGTGAGCCACTACAGCTGTCTGCACG 209
Db 874 ATGATGGTATGGTGGTGGTATC-ACGTGGCTGTGAGCCACTACAGCTGTCTGCACG 815
Qy 210 GTCCCTTCATCAGCCGCGCAGCCAGCGGCGGAGAGAGATGCCCTGTCTCAGAGG 269
Db 814 GTCCCTTCATCAGCCGCGCAGCCAGCGGCGGAGAGAGATGCCCTGTCTCAGAGG 755
Qy 270 ATGCTGTGGCCCTCGGAGAGCAGATGTTCAGGCAACCGAAATCCAGAGCCGACGTTA 329
Db 754 ATGCTGTGGCCCTCGGAGAGCAGATGTTCAGGCAACCGAAATCCAGAGCCGCA-GTYTA 696
Qy 330 CGCCCGGCTCGGCGCCACCGCGCTGGCGGCGGCTTCGCCCGGAGCGGCTT 389
Db 695 CGCCCGGCTCGGCGCCACCGCGCTGGCGGCGGCTTCGCCCGGAGCGGCTT 636
Qy 390 CCACCGCTTCAGCGCCACCTATCCGTAATCTGAGCAGCAGAGATCGACCTGCCACCCACCAT 449
Db 635 CCACCGCTTCAGCGCCACCTATCCGTAATCTGAGCAGCAGAGATCGACCTGCCACCCACCAT 576

3
3
3
4

ORIGIN

	Query Match	Best Local Similarity	77.0%; Score 662.8; DB 13;	Length 850;
	Match	97.9%; Pred No. 5.1e-112;	Mismatches 12;	Indels 3; Gaps 3;
		Conservative 703;		
QY	147	GGTGATGATGGTGGTGTTGGTCATACAGCTGCCTGCTGAGCCACTACAAGCTGCTCTGC	206	
Db	1	GSTGATGATGGTGGTGGTGTTGGTCATCAGTGCCTCGCTGAGCCACTACAAGCTGCTCTGC	60	
QY	207	ACGGTCCTTCATACGCCGCA CAGCCAGGGCGGAGGAGAGATGCCCTGTGCTCTCAGA	256	
Db	61	ACGGTCCTTCATACGCCGCA CAGCCAGGGCGGAGGAGAGATGCCCTGTGCTCTCAGA	120	
QY	267	AGSAGTCCTGTGGCCCTTCGGAGAGCACAGTGTGAGCAAACGGAATCCCAGAGCCGACGCT	336	
Db	121	AGSAGTCCTGTGGCCCTTCGGAGAGCACAGTGTGAGCAAACGGAATCCCAGAGCCGACGCT	180	
QY	327	CTACGCCCGCGCTCGSGCCCCACGACCGCCCTGGGCGCTGCCGCCCTTCGCCACGCGGAGCG	386	
b	181	CTACGCCCGCGCTCGSGCCCCACGACCGCTGGGCGCTGCCGCCCTTCGCCACGCGGAGCG	240	

Query Match	77.0%; Score 662.8; DB 13; Length 850;
Best Local Similarity	97.9%; Pred.No.5.le-112;
Matches 703; Conservative	0; Mismatches 12; Indels 3; Gaps 3;

QY	147	GGTGATGATGGTGGTGATCATCGTCCTGTGAGCCACTACAAGCTGTCTGC	206
DB	1	GGTGATGATGGTGGTGATCATCGTCCTGTGAGCCACTACAAGCTGTCTGC	60
QY	207	ACGFTCCTTCATCAGCCGCCA CAGCCAGSGCGGAGAGAGATGCCCTGTCCCTCAGA	266
DB	61	ACGFTCCTTCATCAGCCGCCA CAGCCAGSGCGGAGAGAGATGCCCTGTCCCTCAGA	120
QY	267	AGGATGCCCTGTGGCCCTCGGAGACGACAGTGTCAAGCAACGGAATCCCAGAGCCGAGGT	326
DB	121	AGGATGCCCTGTGGCCCTCGGAGACGACAGTGTCAAGCAACGGAATCCCAGAGCCGAGGT	180
QY	327	CTACGCCCGCCTCGGCCCA CCGACCGCCTGCGCGCTTCGCCCCAGCGGGAGCG	386
DB	181	CTACGCCCGCCTCGGCCCA CCGACCGCCTGCGCGCTTCGCCCCAGCGGGAGCG	240
QY	387	CTTCCACCGCTTCCAGCCCA CCTATCCGTACCTGACGACGAGATCGACTGCCACCCAC	446
DB	241	CTTCCACCGCTTCCAGCCCA CCTATCCGTACCTGACGACGAGATCGACTGCCACCCAC	300
QY	447	CATTCTGCTGTACAGCGGGAGAGCCCCCA CCTACAGGGGCCCTTGACCCTCCAGCT	506
DB	301	CATTCTGCTGTACAGCGGGAGAGCCCCCA CCTACAGGGGCCCTTGACCCTCCAGCT	360
QY	507	TGGGACCCCGAGCACAGCTGGAATCGAACCGGGAGTGGTGGCGCGACCCCCAAACAG	566
DB	361	TGGGACCCCGAGCACAGCTGGAATCGAACCGGGAGTGGTGGCGCGACCCCCAAACAG	420
QY	567	AACCATTTTCGACAGTGA CTGATGATAGTCCAGGCTGGGGCGGCCCTTGCCCCCCCAG	626
DB	421	AACCATTTTCGACAGTGA CTGATGATAGTCCAGGCTGGGGCGGCCCTTGCCCCCCCAG	480
QY	627	CAGTAACTCGGGCATCAGCGGCCACGCTACGGCAGCGCGGCGCATGAGAGGGCGGCC	686
DB	481	CAGTAACTCGGGCATCAGCGGCCACGCTACGGCAGCGCGGCGCATGAGAGGGCGGCC	540
QY	687	GCCACACTACAGCGAGT CATCGGCCACTACCGCGGCTCTCTTCAGCACCAGCAGAG	746
DB	541	GCCACACTACAGCGAGT CATCGGCCACTACCGCGGCTCTCTTCAGCACCAGCAGAG	600
QY	747	CAGTGGCGCG - CCCTCCTTCTCG - AGGGGACCCGCTCCACCACACACATCGGCC	804
DB	601	CAGTGGCGCGCCCTCTCTCTGTAAGGGACCCGGTTCACCACACACAAATCCGGCC	660
QY	805	CTAGAGAGCGCACCCA - TCTGGAGCAAAGAGATAACAGAAAAGCACCCCTCTC	861
DB	661	CTAAGAGCGCACCCATTCTGGAGCAAGCAGATGATTAACCGAAAGACCCCTCTC	718

RESULT 11	AY419334	780 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	AY419334				
DEFINITION	Homo sapiens TMEMPAI gene, VIRTUAL TRANSCRIPT, partial sequence,				
	genomic survey sequence.				
ACCESSION	AY419334				
VERSION	AY419334.1				
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

AF193334	AV419334	780 bp	DNA	linear	GSS 17-DEC-2003
LOCUS					
DEFINITION	Homo sapiens TMEM1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
ACCESSION	AV419334				
VERSION	AV419334.1	GI:39775291			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

Nature 420, 563-573 (2002)
6 (bases 1 to 1207)

JOURNAL
REFERENCE

Aoachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
Arakawa,T., Bono.H., Carninci,P., Fukuda.S., Fukuishi.Y.,
Furuno.M., Hanagaki.T., Hata.A., Hayatsu.N., Hiramoto.K.,
Hiraka,T., Hori.F., Imotani,K., Iehii,Y., Itoh,M., Izawa,M.,
Kasukawa,T., Kato,H., Kawaj,I., Koijima,Y., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
Nomura,K., Nunasaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa.C.,
Saito,H., Saito.R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Shibata,K., Shibata.Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
Suzuki.H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
Yoshino,M., Muranatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tezurumi-Ku, Yokohama,
Kanagawa 230-0045 Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAAGATTCGGACCTCAAGCGTCTTTTTTTTTTTTVN 3'], cDNA was prepared by using thermostable thermo-activated reverse transcriptase and subsequently prepared for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' CAGAGAATTCTTCGACTTAATAAATATCCGCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
Host: SOLR.

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Location/Qualifiers
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/_db_xref:"MGI:1902457"
/_db_xref:"taxon:10090"
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/sex="male"
/tissue_type="stomach"
/gene_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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/note='unnamed protein product; Nedd4 WW binding protein 4 (MGDI[MGI:192960]) putative'
/codon_start=1
/protein_id="BAB26001.1"
/_db_xref:"GI:12843489"

CDS

/translation="MSPARATQRSFLPPSEITELFEVQIVLVIVVMWMMVTCLLS
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PFPIQSRTQPYPFYQHIALPLPTSLSDGEAPSVYQQFTQLRPDPEOOLINRES
VRAPPNRITFDLDLIDTWLGCPSPSSNGISAIKYCSGSRMEGPPTYSEVIHYGY
GSSFQHQSQNSGSLLGLETRLHHSHAPLENKKEKKQGHPL"

ORIGIN

Query Match 70.1%; Score 603.6; DB 11; Length 1207;
Best Local Similarity 85.2%; Pred. No. 4.6e-101;
Matches 731; Conservative 0; Mismatches 99; Indels 28; Gaps 4;

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Db 340 ACCGC TTGT GTGG GG GT CA CAG CAC CG CC GC CC CC GC CC AT CT TC CT 399
65 GCACGTGC AAC TG -CAA AC GC TCT TTT GTT CCT CAG CAT GGA GA TC AG CG AG CTC GAG TTC 123

Db 705 CGCCCCACCTACAGGCAAGGCATCTGGCCACCTACCCGGGGTCCCTCCTTTTCAGC 762

Search completed: May 12, 2004, 05:18:16
Job time : 2593.37 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 12, 2004, 00:17:12 ; Search time 74.5779 Seconds
(without alignments)
6406.893 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861

Sequence: 1 atgcacgccttgatg999gt.....aacagaaaggacaccctctc 861

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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5: /cgn2_6/ptodata/2/ina/PTCUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	752.8	87.4	759	4	US-09-769-482-2
3	352.2	40.9	921	4	US-09-091-952A-7
4	352.2	40.9	8065	4	US-09-091-952A-6
5	284.2	33.0	867	4	US-09-091-952A-8
6	90.4	10.5	391	4	US-09-621-976-2162
7	48	5.6	696	4	US-09-252-991A-13687
8	48	5.6	1452	4	US-09-252-991A-13650
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11	47.4	5.5	53500	4	US-09-266-985-76
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22	45.4	5.3	424	3	US-08-127-721A-7
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26	44	5.1	44377	2	US-08-804-198-1
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Sequence 1005, Ap
Sequence 1086, Ap
Sequence 7, Appli
Sequence 565, App
Sequence 493, App
Sequence 609, App
Sequence 6427, Ap
Sequence 6203, Ap
Sequence 64, Appl
Sequence 64, Appl

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424 3 US-09-252-991A-1005
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ALIGNMENTS

RESULT 1

US-09-769-482-1

; Sequence 1, Application US/09769482

; Patent No. 6566130

; GENERAL INFORMATION:

; APPLICANT: SRIVASTAVA, SHIV

; APPLICANT: MOUL, JUDD W.

; APPLICANT: XU, LINDA L.

; APPLICANT: SEGAWA, TAKEHIKO

; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY

; FILE REFERENCE: 04995.0057-00000

; CURRENT APPLICATION NUMBER: US/09/769,482

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 60/178,772

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/179,045

; PRIOR FILING DATE: 2000-01-31

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1140

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (95)..(850)

; US-09-769-482-1

Query Match 87.5%; Score 753.6; DB 4; Length 1140;
Best Local Similarity 99.5%; Pred. No. 9e-160;
Matches 756; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 151 GGTGGTGGTGGTATCAGCTGGCTGCTGAGCCACTACAGCTGTCTGCACGGTCTCTATCAG 210
QY 222 CCGGCAAGCAGCGGCGGAGGAGAGAGATGCTGCTCAGAGGATGCTGTGGCC 281
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DB 271 CTGGAGAGCAGAGTGTTCAGGCAACCGGAATCCAGAGCGGAGGCTTACGCGCGGCTCG 330
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Db 631 CAGCGCCAGTGTACGCGAGCG 690
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Qy 762 CTTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 821
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Db 811 CTGGAGCAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 850

RESULT 2

US-09-769-482-2
; Sequence 2, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: POYNUCLEOTIDE ARRAY
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-769-482-2

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Best Local Similarity 99.7%; Pred. No. 1.2e-159;
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Qy 226 CACAGCCAGGGGCGGAGGAGAGATGCGCTTCTCTCAGAAAGATGCTCTGTGGCCCTCG 285
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RESULT 3

US-09-091-952A-7
; Sequence 7, Application US/09091952A
; Patent No. 6458532
; GENERAL INFORMATION:
; APPLICANT: Detera-Wadleigh, Sevilla D.
; Gershon, Elliot S.
; Badner, Judith A.
; Goldin, Lynn R.
; Berrettini, Wade H.
; Yoshikawa, Takeo
; Sanders, Alan R.
; Esterling, Lisa E.

TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/091,952A
 FILING DATE: 19-Apr-1999
 CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/029,278
 FILING DATE: 28-OCT-1996
 APPLICATION NUMBER: PCT/US97/19381
 FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
 NAME: Smith, Timothy L.
 REGISTRATION NUMBER: 35,367
 REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 921 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1...921
 OTHER INFORMATION: Clone 22 coding region
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-091-952A-7

Query Match 40.9%; Score 352.2; DB 4; Length 921;
Best Local Similarity 73.1%; Pred. No. 5.1e-70;
Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

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QY	334	CGCTTCGCGCCACCGACCGCTGCGCGTCCCGCCCTTCGCCAGCGGAGCGCTTCCAC	393
DB	400	GCCCCGCGTCCAGGACAGGTTACAGCGCGCTCTTCATCCAGAGGATCGCTTCAGC	459
QY	394	CGCTTCGCGCCACTTCTGCTACCTGCGACGAGATCGATGCCACCCACCATCTCG	453
DB	460	CGCTTCGCGCCACTTACCCCTATGTGCGACGAGATGATCTCTCTCCACCATCTCC	519
QY	454	CTGTACAGCGGGAGAGCCGCCACCTACCGGGCCCTGACCCCTCCAGCTTCGGGAC	513
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QY	514	CCCGACGAGTGAACCTGAACCGGAGTGGTGGCGGACCCGCCAAGACCATC	573
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QY	574	TTTCAGAGTACCTGATGATGTCAGG---CTGGGCGGCCCTGCCCCCCCCAGCAGT	630
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QY	631	AACTCGGGCATCAGCCCAAGTGTCTACGCGCGCGCGCATGGAGGGCGCGCGGCC	690

DB	700	AACTCGGGCATCAGTCAAGCCTTCAGCATGTAACGGAGGATGAGGGGCCACCCCC	759
QY	691	ACCTACAGCGAGGTCTATCGGCCACTACCGGGGTCTCTTCAGCACCGAGAGCAG	749
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RESULT 4
US-09-091-952A-6
 Sequence 6, Application US/09091952A
 Patent No. 6458532
 GENERAL INFORMATION:
 APPLICANT: Detera-Wadleigh, Sevilla D.
 Gershon, Elliot S.
 Badner, Judith A.
 Goldin, Lynn R.
 Berrettini, Wade H.
 Yoshikawa, Takeo
 Sanders, Alan R.
 Esterling, Lisa E.
 TITLE OF INVENTION: Chromosomal Markers and Diagnostic
 NUMBER OF SEQUENCES: 197
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/091,952A
 FILING DATE: 19-Apr-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/029,278
 FILING DATE: 28-OCT-1996
 APPLICATION NUMBER: PCT/US97/19381
 FILING DATE: 28-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, Timothy L.
 REGISTRATION NUMBER: 35,367
 REFERENCE/DOCKET NUMBER: 015280-297100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8065 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: -
 LOCATION: 1...8065
 OTHER INFORMATION: Clone 22
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 116...1036
 OTHER INFORMATION: Clone 22 coding region
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 452...505
 OTHER INFORMATION: alternatively spliced portion
 FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: 5395...5685
; OTHER INFORMATION: amplified region for genotyping
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-091-952A-6

Query Match          40.9%; Score 352.2; DB 4; Length 8065;
Best Local Similarity 73.1%; Pred. No. 8.5e-70;
Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 94 CAGAGCATGGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCATCGTGTGTGTGATG 153
    |||
Db 281 CGGGGCATCTTCAACTCGGAGCTGGAGTTGCCCAATCATCATCATCGTGTGTGTGTC 340
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QY 154 ATGGTGATGGTGGTGGTGCATCAGCTGCCTGCTGAGCCACTACAAAGCTGCTCGCAGGTC 213
    |||
Db 341 ACGGTATGGTGGTGGTGCATCGTCTGCTGCTGAACCACTACAAAGTCTCCACGGGTCC 400
    |||

QY 214 TTATCAGCGGGCAGCAGCCAGCGGGCGAGGAGAGAGATGCCCTGTCTCTAGAAGATGC 273
    |||
Db 401 TTCATCAACGGGCCGAAACAGAGCCGAGGCGGAGGAGCGGGTGTCCGAGGAAGGGTGC 460
    |||

QY 274 CTGTGGCCCTCGGAGAGACAGATGTCAGGCAACCGAATCCAGAGCGCGAGGCTACGC 333
    |||
Db 461 CTGTGGCCCTCAGACAGCGCCGACCGCGGTGG-----CGCCTCGGAGATCATGCAT 514
    |||

QY 334 CGCCTTCGCCCCACCGAOCGCGCTGCGCGCCCTTCGCGCGGAGAGCGCTTCAC 393
    |||
Db 515 GCCCCGCGTCCAGGAGACAGGTTACAGCGCGCTCTTCATCCAGAGGATCGCTTCAC 574
    |||

QY 394 CGCTTCACGCCCACTATCCGTACCTGCAGACACAGATCGACCTGCCACCACCATCTCG 453
    |||
Db 575 CGCTTCAGGCCCACTACCCCTATGTGCAGACAGAGATGATCTTCTCCACCATCTCC 634
    |||

QY 454 CTGTACAGCGGGAGAGAGCCCCCACTACAGGGCCCTGCAACCTTCAGTTCGGGAC 513
    |||
Db 635 CTGTCCGACGCTGAAGAGCACTCTCTTACCAGGGGCCCTGCACTCTGCAGCTCCGGAC 694
    |||

QY 514 CCGGACACAGCTGAAGCTGAACCGGGAGTCGGTCGCGCACCCCAACAGAACATC 573
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Db 695 CCTGAACAGAGATGGAATCAACCGAGATCCGTGAGGGCCCCCACCAACCGAACATA 754
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QY 574 TTGCACAGTGACCTGATGGATAGTCCACGG---CTGGGGCGGCCCTCCCCCCCAGAGT 830
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Db 755 TTTTGACAGTGAATTAATAGACATTGCTATGTATAGCGGGGTCCATGCCACCCAGCAGC 814
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QY 831 AACTCGGGCATCAGCCCACTGCTACCGCAGCGCGCGGCATGAGAGGGGCGCGCGCC 890
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Db 815 AACTCGGGCATCAGTGCAGACGACCTCTCAGCAGTAAACGGGAGAGTGGAGGGGCCACCCCC 874
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QY 891 ACCTACAGCGAGGTCACTCGGCCACTACCCGGGGTCTCTCTTCCAGCACCGAGAGCAG 749
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Db 933 ACATACAGCGAGGTGATGGGCGACCAACCCAGCGCGCTCTTCTCCATCAACAGCGCAG 933
    |||

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RESULT 5
US-09-091-952A-8
; Sequence 8, Application US/09091952A
; Patent No. 6458532
; GENERAL INFORMATION:
; APPLICANT: Detera-Wadleigh, Sevilla D.
; Gershon, Elliot S.
; Badner, Judith A.
; Goldin, Lynn R.
; Berrettini, Wade H.
; Yoshikawa, Takeo
; Sanders, Alan R.
; Esterling, Lisa E.
; TITLE OF INVENTION: Chromosomal Markers and Diagnostic
; Tests for Manic-Depressive Illness
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1...867
OTHER INFORMATION: clone 22 isoform 2 altered
spliced coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
PS-09-091-952A-8

Query Match	33.0%;	Score	284.2;	DB 4;	Length	867;			
Best Local Similarity	68.7%;	Prod. No.	8.1e-55;						
Matches	453;	Conservative	0;	Mismatches	143;	Indels	63;	Gaps	2;

QY	94	CAGAGCATGGAGATCAGCGAGTGGAGTTGTTTCAGATCATCATCATCGTGGTGTGATG	153
Db	166	CGGGCATCTTCAACTCCGAGCTGGAGTTGCGCCCAATCATCATCATCGTGGTGTGTC	225
QY	154	ATGTGTGATGGTGGTGTGATTCACGTGCTGTGTGAGCCACTCAAGCTCTTTCGACGGTCC	213
Db	226	ACGGTGTGTTGGTGGTGTGATCGTCTGCTGCTCAACCACTACAAAGTCTCCACGGGTCC	285
QY	214	TTATCATCCGGCACACGACCGAGGGCGGAGAGAGATGCCCTGTCTCTCAGAAGGATGC	273
Db	286	TTTCATCAACGCCCGAACCAGACCGGAGCGGGAGACGGCT-----	329
QY	274	CTGTGGCCCTCGGAGAGCACAGTGTTCAGGCAACGGAATCCAGACCGGAGGTTTCACCC	333
Db	330	-----GCCGCAGATCATGCAT	345
QY	334	CGGCTCGGGCCACCGACCGCTGGCGGTCCGCCCTTCGCCACGCGAGGCGCTTCAC	393
Db	346	GCCCGCGGTCCAGGACAGGTTTCAGGCGCGTCTTCATCCAGAGGATCGCTTCAGC	405
QY	394	CGCTTCCAGGCCACCTATCCGTACTCTGCACGACGAGATCGACGTGCCACCCACCACTCG	453
Db	406	CGCTTCCAGGCCACCTACCCCTATGTGCACACGAGATTGATCTTCTCCCAACCATCTCC	465
QY	454	CTGTTCAGACGGGAGGAGCCCCCAACCTACACAGGGCCCTGCACCTCTCAGCTTCGGGAC	513
Db	466	CTGTCCGACGGTGTAGAGAGCACCTCTTACACAGGGGCCCTGCACCTCGAGCTTCGGGAC	525

286	TT	CATCAACGCGCCGACACAGAGCGGAGCGGGCT	329
274	CT	TGGCCCTCGGAGACACAGTGTAGGCACGGHAATCCAGAGCGCAGAGTCTACGCC	333
330	---	-----GCCGCAGATCATGCAT	345
334	CG	CCCTCGGCCACACCGACCGCTGGCGTGGCCGCGAGCGCTTCAC	393
346	GC	CCGCGGTCCAGGACAGGTTACAGCGCGCTTTCATCAGAGGGATCGCTTCAGC	405
394	CG	TTCCAGCGCACTATCCGTACTGTGCACAGAGATCGACTGTGCACCCACCACTCTCG	453
406	CG	CTCCAGCCCACTACCCCTATGTGCACAGAGTTGATCTTCTCCCACTCTCC	465
454	CT	GTGACGGGAGGAGCCCCCACTACACGGGCCCTGCACCTCTCAGCTTCGGGAC	513
466	CT	GTCCGACGGTGAAGAGCACCTCTTACACAGGGGCCCTGCACCTCCGGGAC	525

QY 514 CCCGAGCAGCAGCTGGAACTGAACCGGAGTCCGTGCGCGCACCCCCCAACAGAACCATC 573
Db 526 CCTGAACAGCAGATGGAACCTAACCCGAGATCCGTGAGGGCCCAACCAACCGAACATA 585
QY 574 TTGACAGTACCTGATGATAGTACGAGG---CTGGGCGGCGCCCTGCCCCCCCAGAGT 630
Db 586 TTTGACAGTATGATTTAATAGACATTCCTATGTATAGCGGGGTTCATGCCCAACCCAGCAGC 645
QY 631 AACTCGGCGCATCAGCGCACCTGTACGCGAGCGGGCGCATGGAGGGCGCCGCGCC 690
Db 646 AACTCGGCGCATCAGCGCACCTGTACGCGAGCTGCAGCAGTACCGGAGGATGAGGGGCCACCCCCC 705
QY 691 ACCTACAGCGAGGTCATCGGCCACTACCCGGGTCCTTCCTTCCAGCACCGCAGAGCAG 749
Db 706 ACATACAGCGAGGTCATCGGCCACCAACCCAGCGCTCTTTCTCCATCACCAGCGCAG 764

RESULT 6

US-09-621-976-2162
; Sequence 2162, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2162
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: 17..223
US-09-621-976-2162

Query Match 10.5%; Score 90.4; DB 4; Length 391;
Best Local Similarity 75.7%; Pred. No. 1.5e-11;
Matches 112; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 607 GCGGCCCCCTGCCCCCAGCAGTAACCTCGGCATCAGCGCCACGTGCTACGCGAGCGC 666
Db 26 GGGGTTCATGCCCCCAGCAGCAACTCGGCGATCAGTGAAGACCTGCGAGCAATAC 85
QY 667 GCGCGCATGAGGGGCGCCGCCACCTACAGCGAGGTATCGGCCACTACCCGGGTCC 726
Db 86 GGGAGGATGAGGGGCCACCCCCACATACAGCGAGGTATGGGCCACCAACCCAGCGGCC 145
QY 727 TCTTCCAGCACCAGCAGAGTGGCC 754
Db 146 TCTTCTCCATCACCAGCGCAGAACGC 173

RESULT 7

US-09-252-991A-13687
; Sequence 13687, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13687
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13687

Query Match 5.6%; Score 48; DB 4; Length 696;
Best Local Similarity 57.2%; Pred. No. 0.052;
Matches 87; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 109 ACGGAGCTGGAGTTTGTTCAGATCATCATCTCGTGGTGGTATGATGATGATGATG 168
Db 482 ACCCTGCTGAATCTTCTGTCGATCTGCGCGCGCGTGGTCTTGGCGGTGGTGGT 541
QY 169 GTGATCAGTGTCTCTGAGCCACTACAAGCTGTCTGACCGTCTTCTCATCAGCGGCAC 228
Db 542 CTGGTCAAGCGCTCTGTCGGAAGAAAGAAAGACTGGCTGAGCTGCCATCGCCGCGCAG 601
QY 229 ACCGAGGGCGGAGGAGAGAGATGCCCTGTC 260
Db 602 CGCCATCGCGGAGGCGGATAGCCGCCCTGGC 633

RESULT 8

US-09-252-991A-13650/c
; Sequence 13650, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13650
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13650

Query Match 5.6%; Score 48; DB 4; Length 1452;
Best Local Similarity 57.2%; Pred. No. 0.061;
Matches 87; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 109 ACGGAGCTGGAGTTTGTTCAGATCATCATCTCGTGGTGGTATGATGATGATG 168
Db 267 ACCCTGCTGAATCTTCTGTCGATCTGCGCGCGCGTGGTCTTGGCGGTGGTGGT 208
QY 169 GTGATCAGTGTCTCTGAGCCACTACAAGCTGTCTGACCGTCTTCTCATCAGCGGCAC 228
Db 207 CTGGTCAAGCGCTCTGTCGGAAGAAAGAAAGACTGGCTGAGCTGCCATCGCCGCGCAG 148
QY 229 AGCCAGGGCGGAGGAGAGATGCCCTGTC 260
Db 147 CGCCATCGCGGAGGCGGATAGCCGCCCTGGC 116

RESULT 9

US-07-945-283-1/c
; Sequence 1, Application US/07945283
; Patent No. 5352596
; GENERAL INFORMATION:
; APPLICANT: Cheung, Andrew K.
; APPLICANT: Wesley, Ronald D.
; TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
; TITLE OF INVENTION: Involving The EP0 and LIT Genes
; NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 532596th University Street
CITY: Peoria
STATE: IL
COUNTRY: USA
ZIP: 61604

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/945,283
FILING DATE: 19920911

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
TELEPHONE: 309-685-4011 ext.513
TELEFAX: 309-685-4128

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8438 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Pseudorabies virus

FEATURE:

NAME/KEY: CDS

LOCATION: 622..6495

FEATURE:

NAME/KEY: variation

LOCATION: replace(1099, "g")

FEATURE:

NAME/KEY: variation

LOCATION: replace(1267, "t")

FEATURE:

NAME/KEY: variation

LOCATION: replace(1381, "c")

FEATURE:

NAME/KEY: variation

LOCATION: replace(1566, "c")

FEATURE:

NAME/KEY: variation

LOCATION: replace(7010, "g")

US-07-945-283-1

Query Match 5.6%; Score 47.8; DB 1; Length 8438;

Best Local Similarity 46.4%; Pred. No. 0.1;

Matches 189; Conservative 0; Mismatches 217; Indels 1; Gaps 1;

QY 353 GCCTGGCGCGTCCCGCCCTTCGCCAGCGGGAGCGCTTCACCGCTTCAGCCCACTATC 412

DB 6181 GCCCGGCGCGGCGGCGCTTCGACCCCGGCCACAGCAGCAGCGGTGC 6122

QY 413 CGTACTGCAGCAGATGACCTGCCACCCACCATCTCGTGTACAGCGGGAGGAGC 472

DB 6121 CGCAGCGCGGCACGCGGGGCGCGCTTCOC-CAGCCTCCCCCGCGCGCGCGGTCT 6063

QY 473 CCCACCCCTACAGGGCCCTTGACCCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAAC 532

DB 6062 CGGCG 6003

QY 533 TGAACCGGGAGTCGGTGGCGCGGACCCCCCAACAGAACCATCTTCGACAGTGAACCTGATGG 592

DB 6002 AGCACCGGAGCGCGCTGCTCGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5943

QY 593 ATAGTGCCAGGCTGGGCGGCGCCCTGCCCCCCCCCAGCAGTAAGTCTGGGCGATCAGCGCCACGT 652

DB 5942 TTGGCGCCCGAGAGCGCGCTCTCTCAACCCCACTCCAGCTCCAGTCCACCAACCG 5883

QY 653 GCTACGCGACGCGGCGCGCATGAGAGGGCGCGGCCACCTACAGGAGGTATCGGCC 712

DB 5882 TCGCGCTCGAGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5823

QY 713 ACTACCGGGGTCTCTCTCCAGCACCGCAGCAGCAGTGTGGCGCGCGCGCGCGCGCG 759

DB 5822 GGGACGCGCGGCGCGCGCGCTTCAGAGACAGCGCGCGCGCGCGCGCGCGCGCGCG 5776

RESULT 10

US-09-266-965-42/c

; Sequence 42, Application US/09266965

; Patent No. 6495348

; GENERAL INFORMATION:

; APPLICANT: Sherman, D

; APPLICANT: Mao, Y

; APPLICANT: Varoglu, M

; APPLICANT: He, M

; APPLICANT: Sheldon, P

; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster

; FILE REFERENCE: 600.456US1

; CURRENT APPLICATION NUMBER: US/09/266,965

; CURRENT FILING DATE: 1999-03-12

; EARLIER APPLICATION NUMBER: US 08/624,447

; EARLIER FILING DATE: 1996-08-19

; EARLIER APPLICATION NUMBER: PCT/US94/11279

; EARLIER FILING DATE: 1994-10-06

; EARLIER APPLICATION NUMBER: US 08/133,963

; EARLIER FILING DATE: 1993-10-07

; NUMBER OF SEQ ID NOS: 145

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 42

; LENGTH: 1215

; TYPE: DNA

; ORGANISM: Streptomyces lavendulae

US-09-266-965-42

Query Match 5.5%; Score 47.4; DB 4; Length 1215;

Best Local Similarity 47.2%; Pred. No. 0.08;

Matches 176; Conservative 0; Mismatches 196; Indels 1; Gaps 1;

QY 446 CCATCTCGCTGTACAGCGGGAGGAGCGCCCACTACAGGGCGCTTCACCTCCAGC 505

DB 775 CCACGTGGTGTCTCGTACAGAGAGCGCGGGCGGTGTCTCCACCGTCTCCCGGGC 716

QY 506 TTCGGGACCCGAGCAGCAGCTGGAACTGAACCGGGAGTGGTGGCGGCGACCCCAACA 565

DB 715 CTGGCGCGCGGTGCGGAGGAGCGCGGTCTCCAGTCCGGCGGTGGCTTCGCGCGGTCA 656

QY 566 GAACCATCTTCGACAGTACCTGATGATAGTGCAGGCTGGGCGGCGCTTCGCGCGCGCA 625

DB 655 TCCAGTCGCGGACATCTGTCTCGCGCGCGGACACAGCGCGGCGCACCCAGCAGGTGCA 596

QY 626 GCACTAATCTCGGCGCATACAGCGCCACGTGTACGAGCGGCGGGCGGATGAGAGGGCGCG 685

DB 595 GGGCCACGTCGACAGGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 536

QY 686 CGCCCACTACAGGAGGTGATCGGCCACTACCGGGGTCTCTCTCCAGCAGCAGCAGA 745

DB 535 GGTCCACCAACACCCCGGTGGCTGCGGGATGCGGTGGCGCGGATCCAGC-TGAGCCCG 477

QY 746 GCAGTGGGCGCGCTCTCTTGTGTGGAGGGACCCCGGTCTCCACACACATCGCGCGCC 805

DB 476 ACACCTGCGCAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 417

QY 806 TAGAGAGCGCAGC 818

DB 416 TCCCGGCGCGCGC 404

RESULT 11

US-09-266-965-76
; Sequence 76, Application US/09266965
; Patent No. 6493348
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456051
; CURRENT APPLICATION NUMBER: US/09/266,965
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 08/624,447
; EARLIER FILING DATE: 1996-08-19
; EARLIER APPLICATION NUMBER: PCT/US94/11279
; EARLIER FILING DATE: 1994-10-06
; EARLIER APPLICATION NUMBER: US 08/133,963
; EARLIER FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 53500
; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-09-266-965-76

Query Match 5.5%; Score 47.4; DB 4; Length 53500;
Best Local Similarity 47.2%; Pred. No. 0.2;
Matches 176; Conservative 0; Mismatches 196; Indels 1; Gaps 1;
QY 446 CCAATCTCGTGTACAGCGGGAGAGCCGCCACCTACACAGGCGCCCTCGACCTCCAGC 505
Db 13517 CCACGTGGTGTGCGGTACAGGAAGCGCGGCGGTCTCTCCACCGTCTCCCGGGGC 13576
QY 506 TTCGGACCCCGAGCAGCAGCTGAACTGAACCGGAGTCGGTGCAGCGACCCCAACA 565
Db 13577 CTGGCCGCGCGTGGCGGAGAGCGCGGTCTCAGTCGCGCTGGCCCGGCTCA 13636
QY 566 GAACCATCTTCGACAGTACCTGATGATAGTCCAGGTGGCGGCGCCCTGCCCCCA 625
Db 13637 TCCAGTCCGGGACATCTGCTCGCGCCCGGAGACCGCGGCGCCACCCAGCAGTGCA 13696
QY 626 GCAGTAATCTCGGCATCAGCGCCACGTGCTAAGCGAGCGCGGCGCATGGAGGCGCG 685
Db 13697 GCGCCACGTCACAGGTGCCAGCCCGCAGTTCGAGCAGCGCGCGCCCGGAGCGCG 13756
QY 686 CGCCACCTACAGCGAGGTATCGGCCACTACCGGGGTCTCTTCCAGCACCCAGCAGA 745
Db 13757 GGTGACGAACCAACCGGTGCGGTGCGGATGCGGTGGCCCGATCCAGC-TCAGCCCG 13815
QY 746 GCAGTGGCGCCCTCTTCTGAGGGGACCGGCTCCACACACAGCATGCGCGCCC 805
Db 13816 AACTGCGCAGGTGCCCGCAGCGAGGAGCAGCTCCGCCAGGCGGCGAGCATCGGTGG 13875
QY 806 TAGAGAGCGCAGC 818
Db 13876 TGCCGCGCGCGC 13888

RESULT 12

US-09-252-991A-4586
; Sequence 4586, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4586
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4586

Query Match 5.4%; Score 46.2; DB 4; Length 561;
Best Local Similarity 51.2%; Pred. No. 0.12;
Matches 108; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 417 CCTGCAGCAGCAGATCGACCTGCGCCACCCACCATCTCGCTGTCAGACGGGAGGAGCCCC 476
Db 175 CTGCTGCACCATATCGGCCACCTCTAGAGAGACCCCGCGCAGATCAGCAGGAGGACCT 234
QY 477 ACCCTACAGGGCCCTGCAACCTTCAGCTTCGGAGCCCCGAGCAGCAGCTGGAACTGAA 536
Db 235 GCGCCACGAGGAATTCGGCGCAGCGCTGCTGCGGAGCTGTTCCAGAGTCGGTCTGCA 294
QY 537 CGGGAGTCGGTGGCGGCGACCCCAACAGAACCATCTTCACAGTGCACCTGATGATAG 596
Db 295 GCCGTGCGCTTCACGATATCGGCCAAGCGCTTCTCTGCGGTGAGCCCGAGCTACCA 354
QY 597 TCCAGAGTCGGCGCGCCCTCTGCCCCCGCAGC 627
Db 355 CGCCAGCCTGTGCGCGGCTCTCCCGGCACAGC 385

RESULT 13

US-09-252-991A-4391
; Sequence 4391, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4391
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4391

Query Match 5.4%; Score 46.2; DB 4; Length 1203;
Best Local Similarity 51.2%; Pred. No. 0.15;
Matches 108; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 417 CCTGCAGCAGCAGATCGACCTGCGCCACCCACCATCTCGCTGTCAGACGGGAGGAGCCCC 476
Db 783 CTGCTGCACCATATCGGCCACCTCTAGAGAGACCCCGCGCAGATCAGCAGGAGGACCT 842
QY 477 ACCCTACAGGGCCCTGCAACCTTCAGCTTCGGAGCCCCGAGCAGCAGCTGGAACTGAA 536
Db 843 GCGCCACGAGGAATTCGGCGCAGCGCTGCTGCGGAGCTGTTCCAGAGTCGGTCTGCA 902
QY 537 CGGGAGTCGGTGGCGGCGACCCCAACAGAACCATCTTCACAGTGCACCTGATGATAG 596
Db 903 GCCGTGCGCTTCACGATATCGGCCAAGCGCTTCTCTGCGGTGAGCCCGAGCTACCA 962
QY 597 TCCAGAGTCGGCGGCGCCCTCTGCCCCCGCAGC 627
Db 963 CGCCAGCCTGTGCGCGGCGCTCCCGGCACAGC 993

RESULT 14
US-09-252-991A-4200/c
; Sequence 4200, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4200
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4200

Query Match 5.4%; Score 46.2; DB 4; Length 1611;
Best Local Similarity 51.2%; Pred. No. 0.16;
Matches 108; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 417 CTTGACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGAGGAGCCCG 476
DB 1474 CTTGCTGCAGATATCGGCACCTCTACGAGACCCCGCGCAGATCGACGAGGAGACCT 1415
QY 477 ACCATACAGGGCCCTGACACCTCCAGCTTGGGACCCCGAGCAGAGCTGGAACTGAA 536
DB 1414 GCGCCAGAGAAATCGGGGCGAGCGCTGTCGCGGAGCTGTCCAGAGTCGGTCTGGCA 1355
QY 537 CCGGGAGTGGTGGCGGACCCCGCCAAACAGAACCATCTTCAGACAGTACCTGATGGATAG 596
DB 1354 GCGGTCGCGCTGACAGTATCGGCCAAGGCTTCCTCTGCGCGTGGACCCGAGCTACCA 1295
QY 597 TGCCAGAGCTGGCGGCGCCCTGCCCCCGCCAGC 627
DB 1294 CGCCAGCTGTGCGGCGCTCCCGGCACAGC 1264

RESULT 15
US-08-785-420-1/c
; Sequence 1, Application US/08785420
; Patent No. 6001976
; GENERAL INFORMATION:
; APPLICANT: MacLennan, David H
; APPLICANT: O'Brien, Peter J.
; TITLE OF INVENTION: DIAGNOSIS FOR PORCINE MALIGNANT
; TITLE OF INVENTION: HYPERTHERMIA
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: P.O. Drawer 34009
; CITY: Charlotte,
; STATE: No. 6001976th Carolina 28234
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,420
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,388

FILING DATE: US 08/030,159
APPLICATION NUMBER: 15-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Layton, Jr., Samuel G.
REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 3477-73
TELECOMMUNICATION INFORMATION:
TELEPHONE: 704-377-1561
TELEFAX: 704-334-2014
TELEX: 57-5102
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15378 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: Porcine RYX1 Gene
POSITION IN GENOME:
UNITS: bp
US-08-785-420-1
Query Match 5.4%; Score 46.2; DB 3; Length 15378;
Best Local Similarity 50.7%; Pred. No. 0.27;
Matches 111; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
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QY 385 CGTTTCCACCGTTTCAGCCACCTATCCGTACCTGACGACGAGATCGACCTGCCACCC 444
DB 13269 GGCATGCGCGCGCGCGCGCGCGCTGCTGCGCTGCTGCGCTGCTGCGCGCGCGCG 13210
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QY 505 CTTCCGGGACCCCGAGCAGCGCTGGAACCGGGAG 543
DB 13149 CCGCGCTGCG 13111

Search completed: May 12, 2004, 05:22:02
Job time : 88.5779 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 11, 2004, 21:10:37 ; Search time 3552.51 Seconds
(without alignments)
10504.776 Million cell updates/sec

Title: US-09-934-249-3
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb.htg.*
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- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	861	100.0	861	6	AX392419	Sequence
2	861	100.0	1321	6	AX392417	Sequence
3	861	100.0	4839	9	AF305616	Homo sapi
4	859.4	99.8	1383	6	AX775889	Sequence
5	839.4	97.5	1061	9	BC015918	Homo sapi
6	755.2	87.7	969	6	BD272494	Secrated
7	754.2	87.6	1141	9	AF224278	Homo sapi
8	753.8	87.5	1913	6	BD272544	Secrated
9	753.6	87.5	969	6	BD272514	Secrated
10	753.6	87.5	969	6	BD272515	Secrated
11	753.6	87.5	969	6	BD272516	Secrated
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13	752.8	87.4	759	6	AR336831	Sequence
14	752.6	87.4	1085	6	AX775887	Sequence
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16	752	87.3	1818	9	AY128643	Homo sapi
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18	750.4	87.2	753	6	BD272534	Secrated
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21	546.4	63.5	61505	9	AF305426	Homo sapi
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23	544.4	63.2	1583	6	AX593655	Sequence
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28	460.6	53.5	1713	6	BD272519	Secrated
29	458.2	53.2	648	6	BD272535	Secrated
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34	401.4	46.6	408	6	AX071267	Sequence
35	400.6	46.5	673	6	AX525744	Sequence
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38	373.2	43.3	231930	2	AC134911	Mus muscu
39	353.6	41.1	249554	2	AC139417	Rattus no
40	353.6	41.1	258632	2	AC111878	Rattus no
41	352.2	40.9	921	6	AR233384	Sequence
42	352.2	40.9	8065	6	AR233383	Sequence
43	352.2	40.9	8494	9	AF009424	Homo sapi
44	350	40.7	2170	6	AX713513	Sequence
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ACCESSION	AX392419.1	GI:19700734				
VERSION	AX392419.1					
KEYWORDS						
SOURCE		Homo sapiens (human)				
ORGANISM		Homo sapiens				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
		Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1	Lee, R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. and				
AUTHORS		Turi, T.G.				
TITLE		Diagnosis and treatment of cardiovascular conditions				

JOURNAL	Patent: WO 0216416-A 3 28-FEB-2002;
FEATURES	THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)
source	Location/Qualifiers 1..861
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Dd	1 ATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCCGCGGGCAGCCCAATGTC 60
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Dd	61 TCTTGCACGTGCACCTCAACACGCTCTTTGTTCCAGAGCATGAGATCAGCGAGCTGGAG 120
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Dd	181 CTGCTGAGCCACTACAGAGCTGTCTGCACGCTCTTTCATCAGCCGGCACGCCAGGGGCGG 240
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Dd	421 CAGCAGAGATCGACTGCCACCCACCACTCTCTGCTGTTCAGACGGGAGAGCCCCCACCC 480
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DEFINITION	Sequence 1 from Patent WO0216416.		
ACCESSION	AX392417		
VERSION	AX392417.1	GI:19700732	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Lee, R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. and Turi, T.G.		
JOURNAL	Diagnosis and treatment of cardiovascular conditions		
FEATURES	Patent: WO 0216416-A 1 28-FEB-2002;		
source	THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PRIZER INC. (US)		
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Best Local Similarity	100.0%;	Pred. No. 3.6e-137;	
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QY	121	TTTGTTTCAGATCATCATCATCGTGGTGGTGCATATGATGATGGTGGTGGTGCATCACGTGC	180
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QY	181	CTGCTGAGCCACTACAAGCTGTCTGTCACGCTCCCTTCATCAGCCGGCATCAGCAGGGCGG	240
Db	593	CTGCTGAGCCACTACAAGCTGTCTGTCACGCTCCCTTCATCAGCCGGCATCAGCAGGGCGG	652
QY	241	AGGAGAGAGATGCCCTGTCTCTCAGAGGATCGCTGTGGCCCTCGGAGAGCACAGTGTCA	300
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Qy 841 AAACAGAAAGGACACCCTTCTC 861

Df Db 1161 AAACAGAAAGGACACCCTTCTC 1181

RESULT 4
AX775889 LOCUS 1383 bp mRNA linear PAT 14-JUL-2003
SEQUENCE 159 from Patent WO03048202.
ACCESSION AX775889
VERSION AX775889.1 GI:32693607
KEYWORDS Homo sapiens (human)
SOURCE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS Matsuda,A. and Muramatsu,S.
TITLE NF-kB activating gene
JOURNAL Patent: WO 03048202-A 159 12-JUN-2003;
Asahi Kasei Kabushiki Kaisha (JP)

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ORIGIN

Query Match 99.8%; Score 859.4; DB 6; Length 1383;
Best Local Similarity 99.9%; Pred. No. 6.7e-137;
Matches 860; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 61 TCCTGCAGTGCAGTAAGCTGTTGTTCAGACAGTAGGATCACGGAGCTGGAG 120
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Qy 121 TTTGTTTCAGATCATCATCGTGGTGGTGAATGATGTTGTTGTTGTTGATTGATCATCGTGC 180
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Qy 191 CTGCTGAGCCACTAAGCTGTTCTCAGCGTCCITTATCAGCCGCGACAGCCAGGGCGG 240
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Qy 301 GGCAACGAATCCAGAGCCGAGTCTACGCCCGCCCTCGGCCAACCGACCGCTGCCC 360
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Qy 361 GTGCCGCGCTTCGCCAGCGGAGGCGCTTCCACCGCTTCCAGCCACCTATCCGTACCTG 420
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Best Local Similarity 99.8%; Pred. No. 4.1e-119;
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RESULT 7
AF224278 1141 bp mRNA linear PRI 18-JUL-2000
LOCUS Homo sapiens PMEPAL protein (PMEPAL) mRNA, complete cds.
DEFINITION AF224278
ACCESSION

AF224278.1 GI:9255808
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Xu,L.D., Shanmugam,N., Segawa,T., Sesterhenn,I.A., McLeod,D.G.,
Moul,J.W. and Srivastava,S.
A novel androgen-regulated gene, PMEPAL, located on chromosome
20q13 exhibits high level expression in prostate
Genomics 66 (3), 257-263 (2000)
20334621
10873380
2 (bases 1 to 1141)
Xu,L.D., Shanmugam,N., Segawa,T., Sesterhenn,I.A., McLeod,D.G.,
Moul,J.W. and Srivastava,S.
Direct Submission
Submitted (12-JAN-2000) CPDR, USUHS, 1530 East Jefferson Street,
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PR 01-MAR-1999 US 60/122458
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PI FRASER
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G01N33/15
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Best Local Similarity 99.5%; Pred. No. 7.6e-119;
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PD 26-NOV-2002
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Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C.
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DB 301 ACCTATCGTACCTGACGACGAGATCGACCTGCGCCACCCACCATCTCGCTGTGAGCGGG 360
QY 466 GAGAGCGCCCGACCTACGAGGCGCCCTGCAACCTCTCAGCTTCGGGACCCCGGAGCAG 525
DB 361 GAGAGCGCCCGACCTACGAGGCGCCCTGCAACCTCTCAGCTTCGGGACCCCGGAGCAG 420
QY 526 CTGGAATCTGAACCGGAGTGGTGGCGGACCCCGGAGAGAGAGAGAGAGAGAGAGAGAG 585
DB 421 CTGGAATCTGAACCGGAGTGGTGGCGGACCCCGGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 586 CTGATGTAGTGTGCGGCGGCGCCCTGCGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 645
DB 481 CTGATGTAGTGTGCGGCGGCGCCCTGCGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 646 GCCACGTGCTACGCGACGCGCGCGCATGAGAGGGCGCGCCCGCCACCTACAGCGAGGTC 705
DB 541 GCCACGTGCTACGCGACGCGCGCGCATGAGAGGGCGCGCCCGCCACCTACAGCGAGGTC 600

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Search completed: May 12, 2004, 03:27:05
Job time : 3556.51 secs

Search completed: May 12, 2004, 03:27:05
Job time : 3556.51 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 11, 2004, 21:06:02 ; Search time 599,354 Seconds
(without alignments)
9363.200 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321

Sequence: 1 cgaccgcggtctcggagcga.....ctgcgtaggtgaaaggcag 1321

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002s.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1321	100.0	1321	6	Abk12137 Human cDN
2	1229	93.0	4839	7	Acc49552 Tumour-as
3	1227.4	92.9	1383	9	Adc37326 Nuclear f
4	803.2	60.8	969	3	Aaa75151 CDNA enco
5	802.2	60.7	1140	6	Abk92120 Prostate
6	802.2	60.7	1141	9	Adb75588 Prostate
7	802.2	60.7	1850	7	Acc49536 Tumour-as
8	801.6	60.7	969	3	Aaa75164 CDNA clon
9	801.6	60.7	969	3	Aaa75163 CDNA clon
10	801.6	60.7	1140	9	Aaa75185 CDNA clon
11	801.6	60.7	1061	3	Aad60105 Human and
12	800.6	60.6	1061	3	Aaa47429 Sequence
13	800.6	60.6	1085	9	Adc37324 Nuclear f
14	800.6	60.6	1334	7	Abz36103 Human sec
15	790.4	59.8	1066	4	Aai57868 Human pol
16	767.4	58.1	806	7	Acc49537 Tumour-as
17	760	57.5	1089	4	Aai59654 Human pol
18	616.4	46.7	878	6	Abk12142 Mouse cDN
19	589.2	44.6	1583	6	Abse61424 Prostate
20	493.5	37.4	693	6	Abk12143 Human MIV
21	466.2	35.3	1713	3	Aaa75152 CDNA enco
22	464.5	35.2	1713	3	Aaa75167 CDNA clon
23	464.5	35.2	1713	3	Aaa75166 CDNA clon

24	454.6	35.2	1713	3	Aaa75168	Aaa75168 CDNA clon
25	417.8	31.6	812	2	Aaz52964	Aaz52964 Human pro
26	417	31.6	474	7	Abz84732	Abz84732 Toxicolog
c 27	401.4	30.4	408	5	Aaf65983	Aaf65983 Novel hum
28	400.6	30.3	673	6	Abt09178	Abt09178 Phase-1 R
29	352.2	26.7	8494	5	Aas77304	Aas77304 DNA enco
30	351.6	26.6	937	3	Aaz52507	Aaz52507 Human sec
31	350.4	26.5	1879	5	Aas84503	Aas84503 DNA enco
32	350	26.5	920	6	Abk34251	Abk34251 Human cDN
33	350	26.5	2170	7	Ada52629	Ada52629 Human cod
34	349	26.4	8065	2	Aav38335	Aav38335 Manic-dep
35	349	26.4	8093	6	Abk12145	Abk12145 Human MIV
36	341.8	25.9	475	6	Abk12144	Abk12144 Human MIV
c 37	333.8	25.3	8103	5	Aas77312	Aas77312 DNA enco
c 38	298	22.6	837	6	Abq43498	Abq43498 Oligonuc
39	298	22.5	837	6	Abq43499	Abq43499 Oligonuc
40	284.2	21.5	1496	9	Adc37452	Adc37452 Nuclear f
41	284.2	21.5	8440	5	Aas77305	Aas77305 DNA enco
42	284.2	21.5	8440	6	Abk83477	Abk83477 Human cDN
43	281	21.3	8011	2	Aav38336	Aav38336 Manic-dep
c 44	270.8	20.5	837	6	Abq43501	Abq43501 Oligonuc
45	270.8	20.5	837	6	Abq43500	Abq43500 Oligonuc

ALIGNMENTS

RESULT 1
ABK12137
ID ABK12137 standard; CDNA; 1321 BP.

AC ABK12137;

DT 05-JUN-2002 (first entry)

DE Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.

XX Human; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1;

KW cytosolic; cardiant; cerebroprotective; antiarteriosclerotic;

KW cardiac cell; anti-apoptotic; vascular endothelial cell;

KW cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis;

XX heart failure.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 413..1276

FT /*tag= a

FT /product= "MIVR-1"

FT /note= "This region is specifically claimed in claim 3"

XX WO200216416-A2.

XX 28-FEB-2002.

XX 21-AUG-2001; 2001WO-US026089.

XX 22-AUG-2000; 2000US-0227159P.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.

XX (PFIZ) PFIZER INC.

XX Lee RT, Landschulz KT, Kennedy SP, Thompson JF, Turi TG;

XX WPI, 2002-280912/32.

XX P-PADB; AAU78231.

XX Novel nucleic acid molecule encoding Mechanically Induced Vascular

XX Receptor-1 polypeptide, useful for treating cardiovascular diseases.

XX Claim 2; Page 87-88; 105pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a

CC Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having
 CC cardiac cell anti-apoptotic activity and fragments of it provided they
 CC are not identical to Genbank sequences A1761441.1, A1594390, NM 004338
 CC and A0177461. Also included are expression vectors, host cells, the MIVR-
 CC 1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting
 CC a molecule having cardiac cell anti-apoptotic activity with a candidate
 CC agent, where the molecule is a nucleic acid molecule comprising MIVR-1,
 CC IEX-1, VDU-1, BTG-2 and TIS-11d or its expression product, determining
 CC if the anti-apoptotic activity is modulated and thereby identifying a
 CC modulator. The cardiac cell anti-apoptotic molecules and nucleic acids
 CC of the invention are useful for treating, diagnosing and monitoring
 CC progression of such diseases and disorders as characterized by increased
 CC apoptotic cell-death of vascular endothelial cells e.g. cardiac
 CC hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart
 CC failure. The present sequence encodes human MIVR-1
 XX
 SQ Sequence 1321 BP; 223 A; 493 C; 440 G; 165 T; 0 U; 0 Other;

Query Match 100.0%; Score 1321; DB 6; Length 1321;
 Best Local Similarity 100.0%; Pred. No. 1.9e-198;
 Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CGACCGCGGTCTCGGAGCGAAACCCGATCTCTCGGACTTGAATGAGGAGGAGGCGG 60
 1 CGACCGCGGTCTCGGAGCGAAACCCGATCTCTCGGACTTGAATGAGGAGGAGGCGG 60
 61 CGGCGCGCGCGCGCGGAGGCGCTCGGCTGGGAAAGCTAGCGCAGAGCTAGCCCC 120
 61 CGGCGCGCGCGCGCGGAGGCGCTCGGCTGGGAAAGCTAGCGCAGAGCTAGCCCC 120
 121 GCGCGGAGCGCGCGCGCGCTCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCG 180
 121 GCGCGGAGCGCGCGCGCGCTCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCG 180
 181 AGCG 240
 181 AGCG 240
 241 TGAGCG 300
 241 TGAGCG 300
 301 CTCTCCCG 360
 301 CTCTCCCG 360
 361 CG 420
 361 CG 420
 421 CTGTATGGGGGTCAACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
 421 CTGTATGGGGGTCAACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
 481 GTGCACTGCAACCGCTCTTGTTCAGAGCATGGAGATCAGGAGCTGGAGTTGTCA 540
 481 GTGCACTGCAACCGCTCTTGTTCAGAGCATGGAGATCAGGAGCTGGAGTTGTCA 540
 541 GATCATCATCATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
 541 GATCATCATCATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
 601 CCACTACAGCTGTCTGCAAGCTCTTGTTCAGAGCATGGAGATCAGGAGCTGGAG 660
 601 CCACTACAGCTGTCTGCAAGCTCTTGTTCAGAGCATGGAGATCAGGAGCTGGAG 660
 661 AGATGCGCTGTCTCAGAGGATGCTGTGGCGCTCGGAGAGCAGAGTGTCTAGGCA 720
 661 AGATGCGCTGTCTCAGAGGATGCTGTGGCGCTCGGAGAGCAGAGTGTCTAGGCA 720
 721 AATCCAGAGCGCGAGGTCTACCGCGCGCTCGGCGCGCGCGCGCGCGCGCGCGCG 780
 721 AATCCAGAGCGCGAGGTCTACCGCGCGCTCGGCGCGCGCGCGCGCGCGCGCGCG 780

QY 781 CTTGCGCCAGCGGAGCGCTTCCACCGCTTCCAGGCCACCTATCCGTACCTCAGACGA 840
 Db 781 CTTGCGCCAGCGGAGCGCTTCCACCGCTTCCAGGCCACCTATCCGTACCTCAGACGA 840
 QY 841 GATGACCTGCGACCCACCATCTCGCTGTGACGCGGAGGAGCCGCCACCTACAGG 900
 Db 841 GATGACCTGCGACCCACCATCTCGCTGTGACGCGGAGGAGCCGCCACCTACAGG 900
 QY 901 CCGCTGACCCCTTCCAGCTTTCGGGAGCCCGAGCAGCAGCTTGAACCCGGAGTCGT 960
 Db 901 CCGCTGACCCCTTCCAGCTTTCGGGAGCCCGAGCAGCAGCTTGAACCCGGAGTCGT 960
 QY 961 GCGCGACCCCGCAACAGAACCATCTTGGACAGTACCTGATGGATAGTCCAGGCTGG 1020
 Db 961 GCGCGACCCCGCAACAGAACCATCTTGGACAGTACCTGATGGATAGTCCAGGCTGG 1020
 1021 CGGCGCGCTGCG 1080
 1021 CGGCGCGCTGCG 1080
 1081 GCGCATGGAGGCG 1140
 1081 GCGCATGGAGGCG 1140
 1141 CTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1200
 1141 CTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1200
 1201 CACACATCG 1260
 1201 CACACATCG 1260
 1261 AGGACACCTCTCTAGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
 1261 AGGACACCTCTCTAGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
 1321 G 1321
 1321 G 1321
 RESULT 2
 ACC49552
 ID ACC49552 standard; cDNA; 4839 BP.
 XX ACC49552;
 XX AC ACC49552;
 XX AC ACC49552;
 XX 01-JUL-2003 (first entry)
 XX Tumour-associated antigenic target protein TAT379 SEQ ID NO:119.
 XX Human; tumour-associated antigenic target; TAT; tumour; diagnosis;
 XX cancer; gene; ss.
 XX Homo sapiens.
 XX OS
 XX WO2003024392-A2.
 XX 27-MAR-2003.
 XX 11-SEP-2002; 2002WO-US028859.
 XX 18-SEP-2001; 2001US-0323268P.
 XX 19-OCT-2001; 2001US-0339227P.
 XX 07-NOV-2001; 2001US-0336827P.
 XX 20-NOV-2001; 2001US-0331906P.
 XX 02-JAN-2002; 2002US-0345444P.
 XX 03-APR-2002; 2002US-0369724P.
 XX 19-AUG-2002; 2002US-0404809P.
 XX (GETH) GENENTECH INC.
 XX PA
 XX

Prantz G, Hillan KJ, Phillips HS, Polakis P, Spencer SD;
Williams EW, Wu TD, Zhang Z;
WPI; 2003-354551/33.
DR P-PSDB; ABP97234.
XX
PT New antibodies against tumor-associated antigenic target polypeptide,
PT useful for treating or diagnosing tumors or cancers in mammals, e.g.
PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
PT carcinomas.
XX
XX Claim 2; Fig 119; 285pp; English.
XX
XX ACC49493 to ACC49552 encode the human tumour-associated antigenic target
XX (TAT) proteins given in ABP97175 to ABP97234. The present invention
XX describes an isolated antibody that binds to a polypeptide having at
XX least 90 % sequence identity to any of the 60 150-500 residue amino acid
XX sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking
XX its associated signal peptide, encoded by any of the 60 2000-3000 base
XX pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have
XX cytostatic activity. The antibody can be used for treating or diagnosing
XX tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast
XX cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal
XX cell carcinomas, or thyroid cancer
XX
XX Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;
XX
XX Query Match 93.0%; Score 1229; DB 7; Length 4839;
XX Best Local Similarity 100.0%; Pred. No. 4,6e-184;
XX Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 93 GGAAGCTAGCGGCGAGGCTCAGCCCGCGGGGAGCGCGCCCGCTGCCAGGCCCATTT 152
Db 1 GGAAAGCTAGCGGCGAGGCTCAGCCCGCGGGGAGCGCGCCCGCTGCCAGGCCCATTT 60
QY 153 TTCCGGAGCGCAACCGCGGGGCACTGCCGAGCCCGCGGGGCTGCCAGGGGAGGCGGGG 212
Db 61 TTCCGAGCGCAACCGCGGGGCACTGCCGAGCCCGCGGGGCTGCCAGGGGAGGCGGGG 120
QY 213 GGGCGAGCGAGCGCGTCCCGGCACTGAGCCCGCGCGCCCGCGGAACTTGGCGGC 272
Db 121 GGGCGAGCGAGCGCGTCCCGGCACTGAGCCCGCGCGCGCCCGGAACTTGGCGGC 180
QY 273 GACCCGAGCCGGCGAGCGGGGCGCGCTCCCGCGCGCGCCCTTCGATGCGGGGC 332
Db 181 GACCCGAGCCGGCGAGCGGGGCGCGCTCCCGCGCGCGCGCTTCGATGCGGGGC 240
QY 333 CCCAGTCCGGCGCGCGCGCGAGCCCGCCCGCGCGCCCGCGCGCCCGCGCGCCCGC 392
Db 241 CCCAGTCCGGCGCGCGCGCGAGCCCGCCCGCGCGCCCGCGCGCCCGCGCGCCCGC 300
QY 393 GCGCGCGCGCGCGCGCTTCATGACCGCTTGATGGGGGTCAACAGCACCGCGCGCGCG 452
Db 301 GCGCGCGCGCGCGCGCTTCATGACCGCTTGATGGGGGTCAACAGCACCGCGCGCGCG 360
QY 453 CGCGCGGCGAGCCCAATGCTCTTGCGAGTGCACCTTCGAAACGCTTTTGTTCAGAGCA 512
Db 361 CGCGCGGCGAGCCCAATGCTCTTGCGAGTGCACCTTCGAAACGCTTTTGTTCAGAGCA 420
QY 513 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCTCGTGGTGGTGGTGGTGA 572
Db 421 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCTCGTGGTGGTGGTGGTGA 480
QY 573 TGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 632
Db 481 TGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 540
QY 633 GCGCGCACCGAGGGGCGGAGAGAGATGCCCTGTCTCAGAGAGGATGCTGTGGC 692
Db 541 GCGCGCACCGAGGGGCGGAGAGAGATGCCCTGTCTCAGAGAGGATGCTGTGGC 600
QY 693 CTCGAGAGCACAGTGTTCAGGCAACCGAAATCCAGAGCGCGAGGTTCTACGCCCGCTC 752

XX Matsuda A, Muramatsu S;
 XX WPI: 2003-505282/47.
 DR P-PSDB; ADC37327.
 XX
 PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
 PT useful for treating inflammation, autoimmune diseases, cancers,
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 PT ischaemic disorders.
 XX
 XX Claim 4; SEQ ID NO 159; 938pp; English.
 XX
 CC The present invention relates to novel proteins and their coding
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 CC kappaB). The proteins and their coding sequences are useful for treating
 CC a disease associated with NF-kappaB activation, such as inflammation,
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 CC neurodegenerative diseases, or ischaemic disorders.
 XX
 SQ Sequence 1383 BP; 253 A; 505 C; 440 G; 185 T; 0 U; 0 Other;
 Query Match 92.9%; Score 1227.4; DB 9; Length 1383;
 Best Local Similarity 99.9%; Pred. No. 8.8e-184;
 Matches 1228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 93 GGAAGCTAGCGGAGAGGCTCAGCCCGCGGCGAGCGCGCCGCTCCAGCCGATT 152
 Db 1 GGAAGCTAGCGGAGAGGCTCAGCCCGCGGCGAGCGCGCCGCTCCAGCCGATT 60
 153 TTCCGAGCCACCCCGCGGCACTGCCAGACCCCGCGGCGTCCGAGGAGCGCGGG 212
 Db 61 TTCCGAGCCACCCCGCGGCACTGCCAGACCCCGCGGCGTCCGAGGAGCGCGGG 120
 213 GGGCGCAGCGAGCGGCTCCCGGCACTGAGCCCGCGGCGCCCGGGAACCTGGCGGC 272
 Db 121 GGGCGCAGCGAGCGGCTCCCGGCACTGAGCCCGCGGCGCCCGGGAACCTGGCGGC 180
 273 GACCCGAGCCCGCGGAGCGCGGCGGCTCCCGCGGCGGCGCTCTCTGATCGCGGGC 332
 Db 181 GACCCGAGCCCGCGGAGCGCGGCGGCGCTCCCGCGGCGGCGCTCTCTGATCGCGGGC 240
 333 CCCAGCTCGGGCGCGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 392
 Db 241 CCCAGCTCGGGCGCGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
 393 GCGCGCGCGCGCGCGCTCCATGACCGCTTGATGGGGGTCAACAGACCGCGCGCGCG 452
 Db 301 GCGCGCGCGCGCGCGCTCCATGACCGCTTGATGGGGGTCAACAGACCGCGCGCGCG 360
 453 CGCGCGGCGAGCCCAATGCTCTCTGACGTGCAACAGCTGTTGTTTCCAGAGCA 512
 Db 361 CGCGCGGCGAGCCCAATGCTCTCTGACGTGCAACAGCTGTTGTTTCCAGAGCA 420
 513 TGGAGATCAGCGAGCTGAGGTTGTTTTCAGATCATCATCTGTTGTTGATGATGTTGA 572
 Db 421 TGGAGATCAGCGAGCTGAGGTTGTTTTCAGATCATCATCTGTTGTTGATGATGTTGA 480
 573 TGGTGGTGTATACGTCGCTGTGAGCCACTACAGCTGTCTGACGTCCTTCAATCA 632
 Db 481 TGGTGGTGTATACGTCGCTGTGAGCCACTACAGCTGTCTGACGTCCTTCAATCA 540
 633 GCGGCGACAGCGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 692
 Db 541 GCGGCGACAGCGCGGCGGAG 600
 693 CTTCCGAGAGCAGTGTTCAGGCAACCGGAATCCAGAGCCGCGAGCTCTACGCCCGGCTC 752
 Db 601 CTTCCGAGAGCAGTGTTCAGGCAACCGGAATCCAGAGCCGCGAGCTCTACGCCCGGCTC 660
 753 GGGCCACCGACCGCTGGCGCTGGCGCTTCCCGCAGGGAGCGCTTCCACGCTTCC 812
 Db 661 GGGCCACCGACCGCTGGCGCTGGCGCTTCCCGCAGGGAGCGCTTCCACGCTTCC 720

QY 813 AGCCACCTATCCGTACCTGACGACGAGATCGACCTGCCACCCACCATCTCGTGTGAG 872
 Db 721 AGCCACCTATCCGTACCTGACGACGAGATCGACCTGCCACCCACCATCTCGTGTGAG 780
 QY 873 AGGGGAGAGCCCGCCACCTTACGAGGCGCCCTGACCCCTCCAGCTTCGGGACCCCGAGC 932
 Db 781 AGGGGAGAGCCCGCCACCTTACGAGGCGCCCTGACCCCTCCAGCTTCGGGACCCCGAGC 840
 QY 933 AGCAGCTGGAACCTGAACCGGGAGTGGGTGCGCGCACCCCGCCAAACAGAACCATCTTCGACA 992
 Db 841 AGCAGCTGGAACCTGAACCGGGAGTGGGTGCGCGCACCCCGCCAAACAGAACCATCTTCGACA 900
 QY 993 GTGACCTGATGATAGTGCAGGCTGGGCGGCGCCCTGCCCGCCAGCAGTAACCTCGGCA 1052
 Db 901 GTGACCTGATGATAGTGCAGGCTGGGCGGCGCCCTGCCCGCCAGCAGTAACCTCGGCA 960
 QY 1053 TCAGCGCCACCTGTCTACCGGCGAGCGCGGCGGCGCATGAGGAGGCGCGCCCGCCACCTTACAGCG 1112
 Db 961 TCAGCGCCACCTGTCTACCGGCGAGCGCGGCGGCGCATGAGGAGGCGCGCGCCCGCCACCTTACAGCG 1020
 QY 1113 AGGTATCGGCCACTTACCCGGGCTCTCTCTCCAGCACCAGCAGCAGTGGGCGGCGCT 1172
 Db 1021 AGGTATCGGCCACTTACCCGGGCTCTCTCTCCAGCACCAGCAGCAGTGGGCGGCGCT 1080
 QY 1173 CTTTCTCGAGGGAGCCCGGCTCCACACACACACATCGCGCCCTTACAGAGCGCAGCA 1232
 Db 1081 CTTTCTCGAGGGAGCCCGGCTCCACACACACACATCGCGCCCTTACAGAGCGCAGCA 1140
 QY 1233 TCTGAGCAAGAGAGAGATTAAGAAAGAGACCCCTCTCTAGGTTCCACAGGGGGCC 1292
 Db 1141 TCTGAGCAAGAGAGAGATTAAGAAAGAGACCCCTCTCTAGGTTCCACAGGGGGCC 1200
 QY 1293 GGGCTGGGCTCGTAGGTGAAAGGCGAG 1321
 Db 1201 GGGCTGGGCTCGTAGGTGAAAGGCGAG 1229
 RESULT 4
 AAA75151
 ID AAA75151 standard; cdna; 969 BP.
 XX
 AC AAA75151;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE cdna encoding a human TANGO 261 polypeptide.
 XX
 KW TANGO 266; TANGO 261; TANGO 262; TANGO 267;
 KW cellular proliferation; cellular differentiation; cellular adhesion;
 KW von Willebrand factor-associated disorder; cell trafficking; cancer;
 KW hematopoietic associated disease; atelectasis; pulmonary congestion;
 KW oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
 KW intestinal disorder; spleen associated disease; renal disorder;
 KW cardiovascular disorder; ischemic heart disease; hydrocephalus;
 KW brain herniation; iatrogenic disease; inflammation; meningitis;
 KW Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
 KW multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 6..764
 FT /*tag= a
 FT /product= "TANGO 261"
 FT sig_peptide 6..89
 FT /*tag= b
 FT mat_peptide 90..764
 FT /*tag= c
 XX
 PN WO200052022-A1.
 XX
 PD 08-SEP-2000.

XX 01-MAR-2000; 2000WO-US005226.
 XX 01-MAR-1999; 99US-0122458P.
 XX (MILL-) MILLENNIUM PHEARM INC.
 XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
 XX WPI; 2000-579269/54.
 XX P-PSDB; AAB18449.
 XX Novel human and murine secreted proteins designated TANGO 216, 261, 262,
 XX 266 and 267 useful as modulating agents of cellular processes, e.g. for
 XX treating cancer.
 XX Claim 2; Fig 5; 175pp; English.
 XX The present sequence encodes a human TANGO 261 polypeptide. The
 XX specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO
 XX 267. The TANGO polypeptides can be used to modulate cellular
 XX proliferation, modulate cellular differentiation and/or modulate cellular
 XX adhesion. The proteins can be used to treat any von Willebrand factor-
 XX associated disorder, regulate extracellular matrix structuring, cellular
 XX adhesion, and cell trafficking and/or migration, modulate cellular
 XX interactions, modulate cell adhesion in proliferative disorders, such as
 XX cancer, modulate the proliferation, differentiation, and/or function of
 XX cells that appear in the bone marrow, and leukocytes, treat bone marrow,
 XX blood and hematopoietic associated diseases and disorders, steelectasis,
 XX pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
 XX asthma and bronchiectasis, intestinal disorders, spleen associated
 XX diseases, modulate renal disorders, treat cardiovascular disorders such
 XX as ischemic heart disease, modulate the proliferation, differentiation,
 XX and/or function of bone and cartilage cells and to treat bone and/or
 XX cartilage associated diseases or disorder. They may also be used to treat
 XX disorders associated with the ovaries, cerebral oedema, hydrocephalus,
 XX brain herniations, iatrogenic disease, inflammations, bacterial and viral
 XX meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's
 XX disease, multiple sclerosis, brain cancers, hydrocephalus and
 XX encephalitis, and treat hepatic disorders
 XX
 XX Sequence 969 BP; 211 A; 316 C; 294 G; 148 T; 0 U; 0 Other;
 XX
 XX Query Match 60.8%; Score 803.2; DB 3; Length 969;
 XX Best Local Similarity 99.6%; Pred. No. 2.8e-117;
 XX Matches 805; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 XX 514 GGAGATCAGCGAGCTGGAGTTGTTTCAGATCATCATCTGCTGCTGATGATGATGAT 573
 XX 2 GGGATGGCGAGCTGGAGTTGTTTCAGATCATCATCTGCTGCTGATGATGATGAT 61
 XX
 XX 574 GGTGGTGGTATCATGCTGCTGCTGAGCCACTACAGCTGTGTGACGGTCTCTCATCAG 633
 XX 62 GGTGGTGGTATCATGCTGCTGAGCCACTACAGCTGTGTGACGGTCTCTCATCAG 121
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 XX 634 CCGGCACAGCCAGGGCGGAGAGAGAGATGCTCTCTCAGAGGATGCTGTGGCC 693
 XX 122 CCGGCACAGCCAGGGCGGAGAGAGAGATGCTCTCTCAGAGGATGCTGTGGCC 181
 XX
 XX 694 CTGGAGAGACAGTGTCTAGGCAACCGAATCCAGAGCCGAGGCTACGCCCGGCTCG 753
 XX 182 CTGGAGAGACAGTGTCTAGGCAACCGAATCCAGAGCCGAGGCTACGCCCGGCTCG 241
 XX
 XX 754 GCCACCGAGCCGCTGCGCTGCGCCCTTCGCCAGCGGAGCGCTCCACCGTTCCA 813
 XX 242 GCCACCGAGCCGCTGCGCTGCGCCCTTCGCCAGCGGAGCGCTCCACCGTTCCA 301
 XX
 XX 814 GCCACCTATCCGTACTGTCAGACGAGATGCACTTGCACCCACCATCTCGCTGTGAGA 873
 XX 302 GCCACCTATCCGTACTGTCAGACGAGATGCACTTGCACCCACCATCTCGCTGTGAGA 361
 XX
 XX 874 CGGGAGAGCCCGCCACCTACAGGGCCCTTCACCTCCAGCTTCGGAGCCCGGAGCA 933
 XX

Db 362 CGGGAGGAGCCCCCCCCCTACAGAGGGCCCTTCACCTCCAGCTTCGGAGCCCCGAGCA 421
 Qy 934 GCAGCTGGAACTGAACCGGAGTTCGTGCGCGCACCCCCCAACAGAACCATCTTCGACAG 993
 Db 422 GCAGCTGGAACTGAACCGGAGTTCGTGCGCGCACCCCCCAACAGAACCATCTTCGACAG 481
 Qy 994 TGACCTGTGATAGTGCAGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1053
 Db 482 TGACCTGTGATAGTGCAGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 541
 Qy 1054 CAGCGCCACGTCGTACGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1113
 Db 542 CAGCGCCACGTCGTACGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 601
 Qy 1114 GGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1173
 Db 602 GGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 661
 Qy 1174 CTTGCTGGAGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1233
 Db 662 CTTGCTGGAGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 721
 Qy 1234 CTGGAGCAAGAGAGAGATTAACAGAAAGAGACACCTCTCTAGGCTCCCGAGGGGGCGG 1293
 Db 722 CTGGAGCAAGAGAGAGATTAACAGAAAGAGACACCTCTCTAGGCTCCCGAGGGGGCGG 781
 Qy 1294 GGCTGGGCGGCTGCTAGGTGAAAGGCGAG 1321
 Db 782 GGCTGGGCGGCTGCTAGGTGAAAGGCGAG 809
 XX
 XX RESULT 5
 XX ABK92120
 XX ID ABK92120 standard; DNA; 1140 BP.
 XX AC ABK92120;
 XX XX
 XX DT 15-AUG-2002 (first entry)
 XX DE
 XX XX
 XX KW Prostate cancer-associated DNA sequence #6.
 XX KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
 XX gene therapy; gene; ds.
 XX OS Mammalia.
 XX XX
 XX FN WO200230268-A2.
 XX XX
 XX PD 18-APR-2002.
 XX XX
 XX PF 12-OCT-2001; 2001WO-US032045.
 XX XX
 XX PR 13-OCT-2000; 2000US-00687576.
 XX PR 08-DEC-2000; 2000US-00733288.
 XX PR 08-DEC-2000; 2000US-00733742.
 XX PR 24-JAN-2001; 2001US-0263957P.
 XX PR 16-MAR-2001; 2001US-0276791P.
 XX PR 06-MAR-2001; 2001US-0276888P.
 XX PR 16-MAR-2001; 2001US-0281922P.
 XX PR 24-APR-2001; 2001US-0286214P.
 XX PR 30-APR-2001; 2001US-00847046.
 XX PR 04-MAY-2001; 2001US-0288589P.
 XX XX
 XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX PI
 XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
 XX WPI; 2002-471335/50.
 XX DR P-PSDB; ABG61805.
 XX XX
 XX PT Detecting a prostate cancer-associated transcript in a cell in a patient,
 XX useful for diagnosing prostate cancer (PC) or screening modulators of PC,
 XX by determining if prostate cancer-associated genes are expressed in a

PT prostate tissue.
 PS Claim 22; Page 305; 436pp; English.
 XX The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.
 CC ABX92115-ABX92263 represent prostate cancer-associated polynucleotide sequences
 XX
 SQ Sequence 1140 BP; 270 A; 350 C; 336 G; 184 T; 0 U; 0 Other;
 Query Match 60.7%; Score 802.2; DB 6; Length 1140;
 Best Local Similarity 98.4%; Pred. No. 3.9e-117;
 Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 499 TTGTTCAGAGCATGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 558
 DB 77 TCTCCTGCGAAACAGGCAATGGGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 136
 QY 559 GGTATGATGTGATGGTGGTGTATCATCGTGTCTGTAGCCACTACAAAGCTGTCTGC 618
 DB 137 GGTATGATGTGATGGTGGTGTATCATCGTGTCTGTAGCCACTACAAAGCTGTCTGC 196
 QY 619 ACGGTCTTTCATGACCGCGCACGCCAGGCGCGGAGGAGAGATGCCCTGTCTCAGA 678
 DB 197 ACGGTCTTTCATGACCGCGCACGCCAGGCGCGGAGGAGAGATGCCCTGTCTCAGA 256
 QY 679 AGGATGCTGTGGCTCGGAGACACAGTGTCTAGGCAACGGATCCAGAGCGCGAGGT 738
 DB 257 AGGATGCTGTGGCTCGGAGACACAGTGTCTAGGCAACGGATCCAGAGCGCGAGGT 316
 QY 739 CTAGCGCCCGCTCGGCCACCGACCGCTGTGGCGTGGCGCTTCCGCCAGCGGGAGCG 798
 DB 317 CTAGCGCCCGCTGTGGCGCACCGACCGCTGTGGCGTGGCGCTTCCGCCAGCGGGAGCG 376
 QY 799 CTTCACCGCTTCAGCCCACTATCTGCTACCTGCAGACAGATGACCTGCCACCCAC 858
 DB 377 CTTCACCGCTTCAGCCCACTATCTGCTACCTGCAGACAGATGACCTGCCACCCAC 436
 QY 859 CATCTCGTGTTCAGACGGGGAGGAGCCGCCCTTACAGGGCCCTTGCACCTTCCAGCT 918
 DB 437 CATCTCGTGTTCAGACGGGGAGGAGCCGCCCTTACAGGGCCCTTGCACCTTCCAGCT 496
 QY 919 TCGGACCCCGAGCAGCAGCTGGAATCAACGGGAGTGTGTGGCGGACCCCAACAG 978
 DB 497 TCGGACCCCGAGCAGCAGCTGGAATCAACGGGAGTGTGTGGCGGACCCCAACAG 556
 QY 979 AACCATCTTCAGACGTACCTGATGGATGTCAGGCTGGGGCGGCCCTTCCGCCCGAG 1038
 DB 557 AACCATCTTCAGACGTACCTGATGGATGTCAGGCTGGGGCGGCCCTTCCGCCCGAG 616
 QY 1039 CAGTAATCTCGGCGCATCAGCGCACGTGTACGGAGCGCGGGCGCATGAGGGGCGCGC 1098
 DB 617 CAGTAATCTCGGCGCATCAGCGCACGTGTACGGAGCGCGGGCGCATGAGGGGCGCGC 676
 QY 1099 GCCCACTTACAGCAGGTCATCGGCCACTTACCCGGGTCTTCCCTTCAGACACAGCAGAG 1158
 DB 677 GCCCACTTACAGCAGGTCATCGGCCACTTACCCGGGTCTTCCCTTCAGACACAGCAGAG 736
 QY 1159 CAGTGGCGCGCCCTCTTCTGTGGAGGAGACCGGCTCCACACACACATCGCGCCCT 1218

DB 737 CAGTGGCGCGCCCTCTTCTGTGGAGGACCCGGCTCCACACACACATCGCGCCCT 796
 QY 1219 AGAGAGCGCAGCATCTCTGAGCAAGAGAGAGATAAAGAGAAAGCACCCTCTCTAGG 1278
 DB 797 AGAGAGCGCAGCATCTCTGAGCAAGAGAGAGATAAAGAGAAAGCACCCTCTCTAGG 856
 QY 1279 TCCCCAGGGGGCGGGCTGGGGCTGCTAGGTGAAAAGGCGAG 1321
 DB 857 TCCCCAGGGGGCGGGCTGGGGCTGCTAGGTGAAAAGGCGAG 899
 RESULT 6
 ADB75588
 ID ADB75588 standard; cDNA; 1141 BP.
 XX
 AC ADB75588;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Prostate cancer marker cDNA.
 XX
 KW Prostate; cancer; cytostatic; gene therapy; marker; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003009814-A2.
 XX
 PD 06-FEB-2003.
 XX
 PF 25-JUL-2002; 2002WO-US023913.
 XX
 PR 25-JUL-2001; 2001US-0307982P.
 PR 22-AUG-2001; 2001US-0314356P.
 PR 25-SEP-2001; 2001US-0325020P.
 PR 12-DEC-2001; 2001US-0341746P.
 PR 05-MAR-2002; 2002US-0362158P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
 PI Hoersh S, Kamathar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
 XX
 DR WPI; 2003-248033/24.
 XX
 PT New nucleic acid molecule, useful for diagnosing or treating prostate cancer.
 XX
 PS Disclosure; SEQ ID NO 412; 99pp; English.
 XX
 CC The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer.
 CC Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1141 BP; 271 A; 350 C; 336 G; 184 T; 0 U; 0 Other;
 Query Match 60.7%; Score 802.2; DB 9; Length 1141;
 Best Local Similarity 98.4%; Pred. No. 3.9e-117;
 Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 499 TTGTTCAGAGCATGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 558

542	Db	CAGGCCACGTGCTACGGCAGCGGGCGCATGAGGGCGCGGCCCACTACAGCGA	601
1114	QY	GGTCATCGGCCACTACCCGGGGTCTCTCTTCCAGCACACAGCAGCAGTGGGCGCGCCCTC	1173
602	Db	GGTCATCGGCCACTACCCGGGGTCTCTCTTCCAGCACACAGCAGCAGTGGGCGCGCCCTC	661
1174	QY	CTTGCTTGAGGGGACCGGCTCCACCACACACACATCGCGCCCTTAGAGAGCGCAGCCAT	1233
662	Db	CTTGCTTGAGGGGACCGGCTCCACCACACACACATCGCGCCCTTAGAGAGCGCAGCCAT	721
1234	QY	CTGAGCAAGAGAAAGGATAAACAGAAAGGACACCCCTCTCTAGGGTCCCCCAGGGGGCCG	1293
722	Db	CTGAGCAAGAGAAAGGATAAACAGAAAGGACACCCCTCTCTAGGGTCCCCCAGGGGGCCG	781
1294	QY	GGCTGGGGCTGCGTAGGTGAAAGGCGAG	1321
782	Db	GGCTGGGGCTGCGTAGGTGAAAGGCGAG	809

RESULT 9

AAA75163

ID AAA75163 standard; cDNA; 969 BP.

AC AAA75163;

DT 15-JAN-2001 (first entry)

XX DE cDNA clone encoding a human TANGO 261 polypeptide.

XX	TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
KX	cellular proliferation; cellular differentiation; cellular adhesion;
KW	von Willbrand factor-associated disorder; cell trafficking; cancer;
KW	hematopoietic associated disease; atelectasis; pulmonary congestion;
KW	edema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
KW	intestinal disorder; spleen associated disease; renal disorder;
KW	cardiovascular disorder; ischemic heart disease; hydrocephalus;
KW	brain herniation; latrogenic disease; inflammation; meningitis;
KW	Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
XX	multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
OS	Homio sapiens.

	Key	Location/Qualifiers
FT	CDS	6. .764
FT		/*tag= a
FT		/product= "TANGO 261"

XX PN WO200052022-A1.

08-SEP-2000.
CD
YY

XX
PF 01-MAR-2000: 2000WO-US005226.XX
PR 01-MAR-1999: 99US-0122458P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX
PI Barnes TM, Holtzman DA, Sharp JD, Fraser CC;

XX
DR WPI: 2000-579269/54.

DR WFL; 2000-373269/
DR P-PSDB; AAB18461.

PT Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer.

XX PS Disclosure: Page: 175pp: English.

CC AAA75163-65 encode human TANGO 261 proteins. The specification also
 CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO
 CC polypeptides can be used to modulate cellular proliferation, modulate
 CC cellular differentiation and/or modulate cellular adhesion. The proteins
 CC can be used to treat any von Willebrand factor-associated disorder
 CC
 XX

QY 1234 CTGGAGCAAGAGAGGATTAACAGAAAGGACACCTCTTAGGGTCCCAAGGGGGCGG 1293
 DB 722 CTGGAGCAAGAGAGGATTAACAGAAAGGACACCTCTTAGGGTCCCAAGGGGGCGG 781
 QY 1294 GCTGGGGCTGCTAGGTGAAAGGCAG 1321
 DB 782 GCTGGGGCTGCTAGGTGAAAGGCAG 809

RESULT 10

AAA75165
 ID AAA75165 standard; cDNA; 969 BP.
 AC AAA75165;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE cDNA clone encoding a human TANGO 261 polypeptide.
 XX
 KW TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
 KW cellular proliferation; cellular differentiation; cellular adhesion;
 KW von Willebrand factor-associated disorder; cell trafficking; cancer;
 KW hematopoietic associated disease; atelectasis; pulmonary congestion;
 KW edema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
 KW intestinal disorder; spleen associated disease; renal disorder;
 KW cardiovascular disorder; ischemic heart disease; hydrocephalus;
 KW brain herniation; iatrogenic disease; inflammation; meningitis;
 KW Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
 KW multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 6..764
 FT /*tag= a
 FT /product= "TANGO 261"
 XX
 PN WO200052022-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 01-MAR-2000; 2000WO-US005226.
 XX
 PR 01-MAR-1999; 99US-0122458P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
 XX
 DR WPI: 2000-579269/54.
 DR P-PSDB; AAB18463.
 XX
 FT Novel human and murine secreted proteins designated TANGO 216, 261, 262,
 FT 266 and 267 useful as modulating agents of cellular processes, e.g. for
 FT treating cancer.
 PT
 PS Disclosure; Page; 175pp; English.
 PS
 CC AAA75163-65 encode human TANGO 261 proteins. The specification also
 CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO
 CC polypeptides can be used to modulate cellular proliferation, modulate
 CC cellular differentiation and/or modulate cellular adhesion. The proteins
 CC can be used to treat any von Willebrand factor-associated disorder,
 CC regulate extracellular matrix structuring, cellular adhesion, and cell
 CC trafficking and/or migration, modulate cellular interactions, modulate
 CC cell adhesion in proliferative disorders, such as cancer, modulate the
 CC proliferation, differentiation, and/or function of cells that appear in
 CC the bone marrow, and leukocytes, treat bone marrow, blood and
 CC hematopoietic associated diseases and disorders, atelectasis, pulmonary
 CC congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and
 CC bronchiectasis, intestinal disorders, spleen associated diseases,
 CC modulate renal disorders, treat cardiovascular disorders such as ischemic

CC heart disease, modulate the proliferation, differentiation, and/or
 CC function of bone and cartilage cells and to treat bone and/or cartilage
 CC associated diseases or disorder. They may also be used to treat disorders
 CC associated with the ovaries, and cerebral oedema, hydrocephalus, brain
 CC herniations, iatrogenic disease, inflammations, bacterial and viral
 CC meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's
 CC disease, multiple sclerosis, brain cancers, hydrocephalus and
 CC encephalitis, and treat hepatic disorders. note: the present sequence
 CC does not appear in the specification; it was created using information
 CC provided
 XX
 SQ Sequence 969 BP; 210 A; 317 C; 294 G; 148 T; 0 U; 0 Other;
 Query Match 60.7%; Score 801.6; DB 3; Length 969;
 Best Local Similarity 99.5%; Pred. No. 4.9e-117;
 Matches 804; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 514 GGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGGTGGT 573
 DB 2 GGAGATGGGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGGTGGTGGT 61
 QY 574 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 633
 DB 62 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 121
 QY 634 CCGGCACAGCCAGGGGCGGAGGAGAGAGATCCCTGTCTCAGAAAGATGCTGTGGCC 693
 DB 122 CCGGCACAGCCAGGGGCGGAGGAGAGAGATCCCTGTCTCAGAGCGATGCTGTGGCC 181
 QY 694 CTCGGAGACACAGTGTCTCAGGCAACGGATCCAGAGCGGAGGCTAGCCCGGCTCG 753
 DB 182 CTCGGAGAGACAGTGTCTCAGGCAACGGATCCAGAGCGGAGGCTAGCCCGGCTCG 241
 QY 754 GCCACCCAGCCGCTGGCCGCTGCGCCCTTCGCCAGCGGAGCGCTTCCACCGTTCAC 813
 DB 242 GCCACCCAGCCGCTGGCCGCTGCGCCCTTCGCCAGCGGAGCGCTTCCACCGTTCAC 301
 QY 814 GCCACCTATCCGTACTCTGACGACAGAGATCGACCTGCCACCCACCATCTCGCTGCAG 873
 DB 302 GCCACCTATCCGTACTCTGACGACAGAGATCGACCTGCCCGCCACCATCTCGCTGCAG 361
 QY 874 CGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 933
 DB 362 CGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 421
 QY 934 GCAGCTGGAACTGAACCGGGAGTGGTGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAG 993
 DB 422 GCAGCTGGAACTGAACCGGGAGTGGTGGCGGCGGAGTGGTGGCGGCGGAGTGGTGG 481
 QY 994 TGACCTGATGGATAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1053
 DB 482 TGACCTGATGGATAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 541
 QY 1054 CAGGCGCAGTGTCTCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1113
 DB 542 CAGGCGCAGTGTCTCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 601
 QY 1114 GGTCTATCGGCGCTACCCGCGGCTCTCTTCCAGACACGAGGAGGAGGAGGAGGAGGAG 1173
 DB 602 GGTCTATCGGCGCTACCCGCGGCTCTCTTCCAGACACGAGGAGGAGGAGGAGGAGGAG 661
 QY 1174 CTTCTCTGGAGGAGCCCGGCTCCACACACACATATCGGCGGCGGCGGCGGCGGCGGCGG 1233
 DB 662 CTTCTCTGGAGGAGCCCGGCTCCACACACACATATCGGCGGCGGCGGCGGCGGCGGCGG 721
 QY 1234 CTTGAGCAAGAGAGAGGATTAACAGAAAGGACACCTCTCTAGGGTCCCAAGGGGGCGG 1293
 DB 722 CTTGAGCAAGAGAGAGGATTAACAGAAAGGACACCTCTCTAGGGTCCCAAGGGGGCGG 781
 QY 1294 GGCTGGGGTGGCTAGGTGAAAGGCAG 1321
 DB 782 GGCTGGGGTGGCTAGGTGAAAGGCAG 809


```

RESULT 11
AAD60105
ID AAD60105 standard; cDNA; 1140 BP.
XX
AC AAD60105;
XX
DT 18-DEC-2003 (first entry)
XX
XX Human androgen-regulated gene (ARG), PMEPAL.
DE
XX Human androgen-regulated gene; ARG; PMEPAL; prostate cancer;
KW chromosome 20q13; gene; ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
CDS 95..853
FT /*tag= a
FT /product= "Human PMEPAL protein"
FT /note= "CDS is referred to as SEQ ID NO:2 in claim 1 of
FT the specification"
XX
XX US6566130-B1.
XX
XX 20-MAY-2003.
XX
XX 26-JAN-2001; 2001US-00769482.
XX
XX 28-JAN-2000; 2000US-0178772P.
XX
XX 31-JAN-2000; 2000US-0179045P.
XX
XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
XX Srivastava S, Moul JW, Xu LL, Segawa T;
XX WPI; 2003-719644/68.
XX P-PSDB; AAE39589.
XX
XX Novel isolated androgen-regulated gene designated as PMEPAL useful for
XX selecting primers and probes for detecting prostate cancer cells in
XX biological samples by nucleic acid amplification techniques.
XX
XX Example 7; Col 29-30; 58pp; English.
XX
XX The invention relates to an isolated androgen-regulated gene (ARG)
XX designated as PMEPAL. The invention is useful for selecting primers and
XX probes for detecting prostate cancer cells in a biological sample by
XX using nucleic acid amplification techniques. The present sequence is
XX human PMEPAL cDNA. PMEPAL gene chromosome 20q13
XX
XX Sequence 1140 BP; 271 A; 349 C; 336 G; 184 T; 0 U; 0 Other;
XX
Query Match 60.7%; Score 801.6; DB 9; Length 1140;
Best Local Similarity 99.5%; Pred. No. 4.9e-117;
Matches 804; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 514 GGAGATCACCGAGCTGGAGTTGTCAGATCATCATCGTGGTGGTATGATGAT 573
DB 91 GGCATGCGGAGCTGGAGTTGTTTCAGATCATCATCGTGGTGGTATGATGAT 150
XX
QY 574 GGTGGTGGTATCACGTCCTGTCAGCCACTACAAGCTGTCTGCACGGTCTTCATCAG 633
DB 151 GGTGGTGGTATCACGTCCTGTCAGCCACTACAAGCTGTCTGCACGGTCTTCATCAG 210
XX
QY 634 CCGGCACAGCCAGGGCGGAGAGAGATGTCCTGTCAGAGGATGCTGTGGCC 693
DB 211 CCGGCACAGCCAGGGCGGAGAGAGATGTCCTGTCAGAGGATGCTGTGGCC 270
XX
QY 694 CTCGGAGACACAGTGTTCAGGCAACGGAATCCAGAGCCGCGAGGTCTACGCCCGGCTCG 753
DB 271 CTCGGAGACACAGTGTTCAGGCAACGGAATCCAGAGCCGCGAGGTCTACGCCCGGCTCG 330
XX

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QY 754 GCCCACCGAGCGGCTGCGCGCTTCCGCCAGCGGAGGCGCTTCCACGCTTCCA 813
DB 331 GCCCACCGAGCGGCTGCGCGCTTCCGCCAGCGGAGGCGCTTCCACGCTTCCA 390
XX
QY 814 GCCCACCTATCCGTACCTGAGCAGCAGAGATCGACCTGCCACCCACCACTCTCGTGTGAGA 873
DB 391 GCCCACCTATCCGTACCTGAGCAGCAGAGATCGACCTGCCACCCACCACTCTCGTGTGAGA 450
XX
QY 874 CGGGAGAGCGCCACCCCTACAGGGCGGCTGCACCTCCAGCTTCGGGAGCCCGGAGCA 933
DB 451 CGGGAGAGCGCCACCCCTACAGGGCGGCTGCACCTCCAGCTTCGGGAGCCCGGAGCA 510
XX
QY 934 GCACCTGGAACCTGAACCGGGAGTCGGTGGCGGACCCGCCCAACAGAACCACTTTCGACAG 993
DB 511 GCACCTGGAACCTGAACCGGGAGTCGGTGGCGGACCCGCCCAACAGAACCACTTTCGACAG 570
XX
QY 994 TGACCTGATGATAGTGCACAGGCTGGCGGGCGGCTGCAGCCCGGAGCACTGCGGCAT 1053
DB 571 TGACCTGATGATAGTGCACAGGCTGGCGGGCGGCTGCAGCCCGGAGCACTGCGGCAT 630
XX
QY 1054 CAGCGCCACGTCGTACCGGACGCGGGCGGATGGAGGGCGCGGCCGCCACCTACAGCGA 1113
DB 631 CAGCGCCACGTCGTACCGGACGCGGGCGGATGGAGGGCGCGGCCGCCACCTACAGCGA 690
XX
QY 1114 GGTCACTGGCCACTACCCGGGGTCTCTCTTCAGCACCAGCAGAGAGTGGCGGCCCTC 1173
DB 691 GGTCACTGGCCACTACCCGGGGTCTCTCTTCAGCACCAGCAGAGAGTGGCGGCCCTC 750
XX
QY 1174 CTTGCTGGAGGGGACCCGGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCAT 1233
DB 751 CTTGCTGGAGGGGACCCGGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCAT 810
XX
QY 1234 CTGAGCAAAAGAGAAAGATAAACAGAAAGGACCCCTCTTAGGGTCCCGAGGGGGCGG 1293
DB 811 CTGAGCAAAAGAGAAAGATAAACAGAAAGGACCCCTCTTAGGGTCCCGAGGGGGCGG 870
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QY 1294 G3CTGGG3CTGCTAGGTAGTAAAG3CGAG 1321
DB 871 G3CTGGG3CTGCTAGGTAGTAAAG3CGAG 898
XX
RESULT 12
AAA47429
ID AAA47429 standard; DNA; 1061 BP.
XX
AC AAA47429;
XX
DT 20-OCT-2000 (first entry)
XX
DE Sequence encoding human neuron-associated protein.
XX
KW Neuron associated protein; NEUAP; neurological disorder; epilepsy;
KW ischemic cerebrovascular disease; stroke; cerebral neoplasm;
KW Alzheimer's disease; Pick's disease; Huntington's disease; dementia;
KW Parkinson's disease; demyelinating disease; meningitis; prion disease;
KW kuru; Creutzfeldt-Jakob disease; neurofibromatosis; cerebral palsy;
KW muscular dystrophy; central nervous system; CNS;
KW peripheral nervous system; PNS; myopathy; schizophrenia;
KW actinic keratosis; arteriosclerosis; atherosclerosis; bursitis;
KW cirrhosis; hepatitis; mixed connective tissue disease; MCTD;
KW myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer;
KW autoimmune disease; inflammation; acquired immunodeficiency syndrome;
KW AIDS; Addison's disease; adult respiratory distress syndrome; allergy;
KW ankylosing spondylitis; amyloidosis; anaemia; asthma;
KW Werner syndrome; trauma; human; ds.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
CDS 101..859
FT /*tag= a
FT /product= "Neuron associated protein"
XX

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XX Matsuda A, Muramatsu S;
 XX WPI: 2003-505282/47.
 DR P-PSDB; ADC37325.
 XX
 PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
 PT useful for treating inflammation, autoimmune diseases, cancers,
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 PT ischemic disorders.
 XX
 XX Claim 4; SEQ ID NO 157; 938pp; English.
 PS
 CC The present invention relates to novel proteins and their coding
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 CC kappaB). The proteins and their coding sequences are useful for treating
 CC a disease associated with NF-kappaB activation, such as inflammation,
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 CC neurodegenerative diseases, or ischemic disorders.
 XX
 SQ Sequence 1085 BP; 223 A; 352 C; 334 G; 176 T; 0 U; 0 Other;
 Query Match 60.6%; Score 800.6; DB 9; Length 1085;
 Best Local Similarity 99.3%; Pred. No. 7e-117;
 Matches 809; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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 AC ABZ36103;
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 DT 10-FEB-2003 (first entry)
 XX
 DE Human secretory polynucleotide SPTM SEQ ID NO 267.
 XX
 XX Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;
 XX asthma; Crohn's disease; neurological disorder; epilepsy; cancer;
 XX Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
 XX multiple sclerosis; Parkinson's disease; cell proliferative disorder;
 XX anti-inflammatory; immunosuppressive; neuroprotective; nontropic;
 XX neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;
 XX antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus;
 XX secretory polynucleotide; secretory protein; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200283876-A2.
 XX
 XX 24-OCT-2002.
 XX
 XX 27-MAR-2002; 2002WO-US009921.
 XX
 XX 29-MAR-2001; 2001US-0280067P.
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 XX 29-MAR-2001; 2001US-0280068P.
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 XX 16-MAY-2001; 2001US-0291280P.
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 XX 17-MAY-2001; 2001US-0291829P.
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 XX 17-MAY-2001; 2001US-0291849P.
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 XX 19-JUN-2001; 2001US-0299428P.
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 XX 20-JUN-2001; 2001US-029976P.
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 XX 20-JUN-2001; 2001US-030001P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 XX Duffour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
 XX Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
 XX Peralta CH, David KH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 XX Flores V, Matwaha R, Lo A, Lan RY, Urashka ME;
 XX
 XX WPI: 2003-075543/07.
 XX
 XX P-PSDB; ABP75860.
 XX
 XX New human secretory proteins and polynucleotides, useful for diagnosing,
 XX treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),
 XX neurological disorders (e.g. Alzheimer's), or cell proliferations or
 XX cancers.
 XX
 XX Claim 1; SEQ ID NO 267; 459pp + Sequence Listing; English.
 PS
 XX
 XX The invention relates to a secretory polynucleotide (designated sptm)
 XX comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a
 XX naturally occurring polynucleotide sequence at least 90 % identical to
 XX the polynucleotide sequence, a polynucleotide complementary to them or an
 XX RNA equivalent of them. The polypeptide or polynucleotide are useful for
 XX treating, preventing or diagnosing a disease or condition associated with
 XX the expression of functional SPTM. These are particularly useful for
 XX diagnosing, treating or preventing autoimmune/inflammatory disorders
 XX (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's

CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,
CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,
CC schizophrenia or amnesia), or cell proliferative disorders (e.g.
CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,
CC breast, cervix or prostate). Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1334 BP; 299 A; 381 C; 394 G; 260 T; 0 U; 0 Other;
Query Match 60.6%; Score 800.6; DB 7; Length 1334;
Best Local Similarity 98.3%; Pred. No. 6.9e-117;
Matches 809; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 499 TTGTTCCAGACATGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCGTGGT 558
DB 82 TCTCTCGGAAACACAGGCAATGGCGAGCTGGAGTTGTTTCAGATCATCATCGTGGT 141
QY 559 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 618
DB 142 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 201
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QY 679 AGGATGCTGTGGCTCGGAGAGACAGTGTGAGGCAAGCAATCCAGAGCGCGAGT 738
DB 262 AGGATGCTGTGGCTCGGAGAGACAGTGTGAGGCAAGCAATCCAGAGCGCGAGT 321
QY 739 CTACGCGCCGCTTGGGCGCCAGCGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 798
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QY 799 CTTCCACCGCTTCCAGCGCCACCTATCCGTACCTGAGCAGCAGATCGACCCACCC 858
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AC AA157868;
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DT 22-OCT-2001 (first entry)
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DE Human polynucleotide SEQ ID NO 71.
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KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
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PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00489725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR P-PSDB; AAM38712.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Claim 1; SEQ ID NO 71; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 1066 BP; 225 A; 348 C; 325 G; 168 T; 0 U; 0 Other;
Query Match 59.8%; Score 790.4; DB 4; Length 1066;
Best Local Similarity 99.2%; Pred. No. 2.8e-115;
Matches 794; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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5	861	65.2	861	6	AX392419	AX392419 Sequence
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ALIGNMENTS

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LOCUS

DERIVATION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

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Lee,R.T., Landeschulz,K.T., Kennedy,S.P., Thompson,J.F. and

Turi,T.O.

Diagnosis and treatment of cardiovascular conditions

AX392417 Sequence 1 from Patent WO0216416.
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AX392417.1 GI:19700732

AX392417 linear PAT 23-MAR-2002

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Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 0216416-A 1 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)
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ORIGIN
Query Match 100.0%; Score 1321; DB 6; Length 1321;
Best Local Similarity 100.0%; Pred. No. 1.6e-176;
Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1321 G 1321

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LOCUS Homo sapiens STAG1/PMEP1 mRNA, complete cds.
DEFINITION AF305616
ACCESSION AF305616
VERSION AF305616.1 GI:16303741
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4839)
AUTHORS Rae, F.K., Hooper, J.D., Nicol, D.I. and Clements, J.A.
TITLE Characterization of a novel gene, STAG1/PMEP1, up-regulated in
renal cell carcinoma and other solid tumors
JOURNAL Mol. Carcinog. 32 (1), 44-55 (2001)
MEDLINE 21453682
PUBMED 11568975
REFERENCE 2 (bases 1 to 4839)
AUTHORS Rae, F.K., Hooper, J.D., Nicol, D.I. and Clements, J.A.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-2000) Centre for Molecular Biotechnology,
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Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 1.1e-163;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
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LOCUS
DEFINITION
Sequence 159 from Patent WO03048202.
ACCESSION
AX775889
VERSION
AX775889.1 GI:32693607
KEYWORDS
SOURCE
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
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Matsuda, A. and Muramatsu, S.
NF-kB activating Gene
Patent: WO 03048202-A 159 12-JUN-2003;
Asahi Kasei Kabushiki Kaisha (JP)
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ORIGIN
Query Match 92.9%; Score 1227.4; DB 6; Length 1383;
Best Local Similarity 99.9%; Pred. No. 2.3e-163;
Matches 1228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 29 Row: e Column: 5
 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

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AX392419	LOCUS	AX392419	861 bp	DNA	linear	PAT 23-MAR-2002
	DEFINITION	Sequence 3 from Patent WO0216416.				
	ACCESSION	AX392419				
	VERSION	AX392419.1	GI:19700734			

KEYWORDS

SOURCE	ORGANISM
Homo sapiens (human)	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Lee, R. T., Landschulz, K. T., Kennedy, S. P., Thompson, J. F. and Turi, T. G.

TITLE

JOURNAL
Patent: WO 0216416-A 3 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)

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QY 1294 GGCTGGGGCTGCGTAGTGAAAGGCGAG 1321
Db 782 GGCTGGGGCTGCGTAGTGAAAGGCGAG 809

RESULT 7
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DEFINITION AF224278
ACCESSION AF224278.1 GI:9255808
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1141)
AUTHORS Xu, L.L., Shanmugam, N., Segawa, T., Sesterhenn, I.A., McLeod, D.G., Moul, J.W., and Srivastava, S.
TITLE A novel androgen-regulated gene, PMEPA1, located on chromosome 20q13 exhibits high level expression in prostate
JOURNAL Genomics 66 (3), 257-263 (2000)
MEDLINE 20334621
PubMed 10873380

REFERENCE 2 (bases 1 to 1141)
AUTHORS Xu, L.L., Shanmugam, N., Segawa, T., Sesterhenn, I.A., McLeod, D.G., Moul, J.W., and Srivastava, S.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-2000) CPDR, USUHS, 1530 East Jefferson Street, Rockville, MD 20852, USA

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QY 1099 GCCCACTTACAGCGAGGTTCATCGGCCCATACCCCGGGTTCCTCTTCAGACACCCAGCAG 1158
Db 677 GCCCACTTACAGCGAGGTTCATCGGCCCATACCCCGGGTTCCTCTTCAGACACCCAGCAG 736
QY 1159 CAGTGGGCGGCCCTCTCTGTCTGGAGGGAGCCCGGCTCCACACACATCGCGCCCT 1218
Db 737 CAGTGGGCGGCCCTCTCTGTCTGGAGGGAGCCCGGCTCCACACACATCGCGCCCT 796
QY 1219 AGAGAGCCCGCATCTCGAGCAAGAGAGATAAACAGAAAGACACCCCTCTCTAGGG 1278
Db 797 AGAGAGCCCGCATCTCGAGCAAGAGAGATAAACAGAAAGACACCCCTCTCTAGGG 856
QY 1279 TCCCGAGGGGCGCGGCTGGGCTGGGTAGGTGAAAGGCGAG 1321
Db 857 TCCCGAGGGGCGCGGCTGGGCTGGGTAGGTGAAAGGCGAG 899

RESULT 8
BD272544 1913 bp DNA linear PAT 17-JUL-2003
LOCUS Secreted proteins and nucleic acids encoding them.
DEFINITION BD272544
ACCESSION BD272544
VERSION BD272544.1 GI:33082312
KEYWORDS JP 2002539773-A/53.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1913)
AUTHORS Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C.
TITLE Secreted proteins and nucleic acids encoding them
JOURNAL Patent: JP 2002539773-A 53 26-NOV-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
FN JP 2002539773-A/53
PF 26-NOV-2002
PI 01-MAR-2000 JP 2000602247
PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C
PI FRASER
PI C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC
GOIN33/15,

[illegible]

RESULT_9	
BD272514	699 bp DNA linear PAT 17-JUL-2003
LOCUS	
DEFINITION	Secreted proteins and nucleic acids encoding them.
ACCESSION	BD272514
VERSION	BD272514.1 GI:33082282
KEYWORDS	JP 2002539773-A/23.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 969)
JOURNAL	Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C. Secreted proteins and nucleic acids encoding them Patent: JP 2002539773-A 23 26-NOV-2002; MILLENNIUM PHARMACEUTICALS INC
COMMENT	OS Homo sapiens (human) PN JP 2002539773-A/23 PD 26-NOV-2002 JP 2000602247 PR 01-MAR-2000 JP 60/122458 FR 01-MAR-1999 US 60/122458 PI THOMAS M BARNES,DOUGLAS A HOLTZMAN,JOHN D SHARP,CHRISTOPHER C FRASER PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/68, PC GOIN33/15, PC GOIN33/50,GOIN33/53,GOIN33/53,GOIN33/566,C12N15/00,C12N5/00 CC Secreted proteins and nucleic acids encoding them FH key Location/Qualifiers FT CDS Location/Qualifiers (6)..(761).
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Query Match	60.7%; Score 801.6; DB 6; Length 969;
Best Local Similarity	99.5%; Pred.No.1.9e-103;
Matches 804; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
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QY	574 GTGTGTGTGTATCAGTGCCTGTGTGAGCCACTACAAGCTGTCTGCACGGTCCCTTCATCAG 633
Db	62 GGTGGTGGTGATCACGTGCTGTGTGAGCCACTACAAGCTGTCTGCACGGTCCCTTCATCAG 121
QY	634 CCGGCACAGCCAGGGCGGAGGAGAAGATGCCCTGTCTCTCAGAAGATGCTCTGTGGCCC 693
Db	122 CCGGCACAGCCAGGGCGGAGGAGAAGATGCCCTGTCTCTCAGAAGATGCTCTGTGGCCC 181
QY	694 CTGGAGAGACAGTAGTGTACGCACACGGATCCAGAGCCGAGGTTCTACGCCCGCCCTCG 753
Db	182 CTGGAGAGACAGTAGTGTACGCACACGGATCCAGAGCCGAGGTTCTACGCCCGCCCTCG 241
QY	754 GCCCACCGAGCCCTGGCCCGTGCCTGGCCCTTCGCCCGAGCGGTCCTTCCACCGCTTCCA 813
Db	242 GCCCACCGAGCCCTGGCCCGTGCCTGGCCCTTCGCCCGAGCGGTCCTTCCACCGCTTCCA 301
QY	814 GCCACCTATTCCGTACTGTGACACAGCATCGACCTGCCACCACCATCTCGCTGTGAGA 873
Db	302 GCCACCTATTCCGTACTGTGACACAGCATCGACCTGCCACCACCATCTCGCTGTGAGA 361
QY	874 CGGGGAGGAGCCCCACCTTACAGGGGCCCTTGACCCCTCCAGCTTCGGGACCCCGAGCA 933
Db	362 CGGGGAGGAGCCCCACCTTACAGGGGCCCTTGACCCCTCCAGCTTCGGGACCCCGAGCA 421
QY	934 GCAGCTGGAACTGAACCGGGAGTGGTGGCGGACACCCGCAACAGAACCACTCTTCGACAG 993
Db	422 GCAGCTGGAACTGAACCGGGAGTGGTGGCGGACACCCGCAACAGAACCACTCTTCGACAG 481
QY	994 TGACCTGATGGATAGTGCCAGGTGGSGCGCCCTGCTGCCCCCAGCAGTAGTACTCGGGCAT 1053

PC	G01N33/50,G01N33/53,G01N33/53,G01N33/566,C12N15/00,C12N5/00	CC
	Secreted proteins and nucleic acids encoding them	PH
	Location/Qualifiers	Key
FT	CDS	
	Location/Qualifiers	
	(5). (761).	
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ORIGIN

	Query Match	60.7%	Score	801.6;	DB	6;	Length	969;
	Best Local Similarity	99.5%;	Pred.	No.	1.9e-103;			
	Matches	804;	Conservative	0;	Mismatches	4;	Indels	0; Gaps
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Dd	2	GGAGATGCGGAGCTGGAGTTGTTTCAGATCATCATCATCGTGTGTTGATGATGGTGAT	61					
Qy	574	GTTGGTGGTGTACAGTGCCTGCTTGAGCCACTACAAGCTGCTCAAGTCTCCTCAGAGGATGCCCTGTGGCC	633					
Dd	62	GTTGGTGGTGTACAGTGCCTGCTTGAGCCACTACAAGCTGCTCAGCGTCTTCATCAG	121					
Qy	634	CCGGCACACCCAGGGGGGAGGAGAGAAGATGCCCTGTCTCAGAAAGGATGCCCTGTGGCC	693					
Dd	122	CCGGCACACCCAGGGGGGAGGAGAGAAGATGCCCTGTCTCAGACGGATGCCCTGTGGCC	181					
Qy	694	CTCGGAGAGCAGTGTTCAGACACAGGAATCCCAGAGCCGAGAGTCTACGCCCGCCCTCG	753					
Dd	182	CTCGGAGAGCAGTGTTCAGGCAACGGAATCCCAGAGCCGAGAGTCTACGGCCGCCCTCG	241					
Qy	754	GCCACCGACCCCTGGCCGTGCGGCCCTTCGCCCGAGGGAGGGCTTCCAACGGTTCCA	813					
Dd	242	GCCACCCAGCCCTGGCCGTGCGGCCCTTCGCCCGAGGGAGGGCTTCCAACGGTTCCA	301					
Qy	814	GCCACCTATCCGTACCTGTCAGCAGCAGATGCACCTGCCACCACCACTCTCGCTGTGAGA	873					
Dd	302	GCCACCTATCCGTACCTGTCAGCAGCAGATGCACCTGCCGCCCACTCTCGCTGTGAGA	361					
Qy	874	CGGGAGAGGCCCCCACCCCTTACAGGGGCCCTTGACCTTCAGCTTCGGGZACCCCGAGCA	933					
Dd	362	CGGGAGAGGCCCCCACCCCTTACAGGGGCCCTTGACCTTCAGCTTCGGGZACCCCGAGCA	421					
Qy	934	GCAGCTGGAATCGAACCCGGGAGTCCGGTCGCGSCACCCCAACAGAAACATCTTCGACAG	993					
Dd	422	GCAGCTGGAATCGAACCCGGGAGTCCGGTCGCGSCACCCCAACAGAAACATCTTCGACAG	481					
Qy	994	TGACCTGATGATAGTGCAGAGCTGGGCGGCCCTTGCCCTCCACAGCAGTAATCTGGGGAT	1053					
Dd	482	TGACCTGATGATAGTGCAGAGCTGGGCGGCCCTTGCCCTCCACAGCAGTAATCTGGGGAT	541					
Qy	1054	CAGCCGCCACGTCTACTAGGCAGGGGGGGCGCATGGAGGGGGCGCGCCACCTACAGCGA	1113					
Dd	542	CAGCCGCCACGTCTACTAGGCAGGGGGGGCGCATGGAGGGGGCGCGCCACCTACAGCGA	601					
Qy	1114	GGTCATCGGCCACTACCCGGGGTCTCTCTTCAGCACCAGAGCAGTGGGCGCGCCCTC	1173					
Dd	602	GGTCATCGGCCACTACCCGGGGTCTCTCTTCAGCACCAGAGCAGTGGGCGCGCCCTC	661					
Qy	1174	CTTGCTGGAGGGGACCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCAT	1233					
Dd	662	CTTGCTGGAGGGGACCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCAT	721					
Qy	1234	CTGGAGCAGAAGAGAGGATAACAGAAAGGACACCCCTCTCTAGGCTGCCCGGGGGCGG	1293					
Dd	722	CTGGAGCAGAAGAGAGGATAACAGAAAGGACACCCCTCTCTAGGCTGCCCGGGGGCGG	781					
Qy	1294	GCGTGGGCTCGCTAGGTGAAAAGGCAG	1321					
Dd	782	GCGTGGGCTCGCTAGGTGAAAAGGCAG	809					

RESULT 12


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Db      811 CTGAGCAAGAAAGAGATAAAGAGACACCTCTCTAGGTGCCCAAGGGGGCG 870
QY      1294 GGCTGGGGCTGCTAGGTGAAAAGGCAG 1321
Db      871 GGCTGGGGCTGCTAGGTGAAAAGGCAG 898

RESULT 13
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LOCUS      AX775887      1085 bp      mRNA      linear      PAT 14-JUL-2003
DEFINITION Sequence 157 from Patent WO03048202.
ACCESSION AX775887
VERSION   AX775887.1 GI:32693605
KEYWORDS Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Matsuda, A. and Muramatsu, S.
TITLE     NF-kB activating gene
JOURNAL   Patent: WO 03048202-A 157 12-JUN-2003;
            Asahi Kasei Kabushiki Kaisha (JP)
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ORIGIN
Query Match      60.6%; Score 800.5; DB 6; Length 1085;
Best Local Similarity 98.3%; Pred No. 2.5e-103;
Matches 809; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      499 TTTGTTCCAGAGCATGAGATCACGGAGCTGGAGTTGTTTTCAGATCATCATCGTGGT 558
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QY      559 GGTGATGATGTGATGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 618
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QY      619 ACGGTCTTCATGACCGGCACAGCCAGCGGCGGAGGAGAGAGATGCCCTGTCTCCTCAGA 678
Db      229 ACGGTCTTCATGACCGGCACAGCCAGCGGCGGAGGAGAGATGCCCTGTCTCCTCAGA 288
QY      679 AGGATGCTGTGGCTTCGGAGAGACAGTGTTCAGGCAACGGATCCAGACGGCGAGGT 738
Db      289 AGGATGCTGTGGCTTCGGAGAGACAGTGTTCAGGCAACGGATCCAGACGGCGAGGT 348
QY      739 CTACGCCCCGCTCGGCCACACCGACCGCTGCGCGCTGCGCGCTTCGCCACGCGGAGCG 798
Db      349 CTACGCCCCGCTCGGCCACACCGACCGCTGCGCGCTGCGCGCTTCGCCACGCGGAGCG 408
QY      799 CTTCCACCGCTTCAGCCGACCACTATCCGTACTCGAGACACAGATCGACCTGCCACCCAC 858
Db      409 CTTCCACCGCTTCAGCCGACCACTATCCGTACTCGAGACACAGATCGACCTGCCACCCAC 468
QY      859 CATCTCGTGTTCAGACGGGAGGAGCCCCACCTTACAGGGCCCCCTGACCCCTCCAGCT 918
Db      459 CATCTCGTGTTCAGACGGGAGGAGCCCCACCTTACAGGGCCCCCTGACCCCTCCAGCT 528
QY      919 TCGGACCCCGAGCAGCAGCTGGAACTGAACCGGAGTCGCTGCGCGCAACCCCAACAG 978

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Db      529 TCGGGACCCCGAGCAGCAGCTGGAACCTGGAGTGGGTGGCGGACCCCAACAG 588
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QY      1099 GCCCACCTACAGCAGGAGTGCATCGGCCACTACCCGGGGTCTCTCTCCAGACACCATGAGCAG 1158
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QY      1159 CAGTGGGCGCGCTCTCTCTGCTGGAGGAGACCGGCTCCACACACACATCGCGCCCT 1218
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QY      1219 AGAGAGCGCAGCCATCTGGAGCAAGAGAGAGATAAACAAGAGACACCCCTCTCTAGGG 1278
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QY      1279 TCCCGAGGGGCGCGGCTGGGGTGGGTAGGTGAAAGGCAG 1321
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RESULT 14
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LOCUS      AX128643      1818 bp      mRNA      linear      PRI 10-APR-2003
DEFINITION Homo sapiens PMEPAL variant A protein mRNA, complete cds.
ACCESSION AX128643
VERSION   AX128643.1 GI:22121998
KEYWORDS Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1818)
AUTHORS   Brunschwig, E.B., Wilson, K., Mack, D., Dawson, D., Lawrence, E.,
            Willson, J.K.V., Lu, S., Nosrati, A., Rerko, R.M., Swinier, S., Beard, L.,
            Lutterbaugh, J.D., Willis, J., Platzner, P., and Markowitz, S.
TITLE     PMEPAL, a transforming growth factor-beta-induced marker of
            terminal colonocyte differentiation whose expression is maintained
            in primary and metastatic colon cancer
            Cancer Res. 63 (7), 1568-1575 (2003)
JOURNAL   22557253
MEDLINE   12670906
REFERENCE 2 (bases 1 to 1818)
AUTHORS   Brunschwig, E.B., Wilson, K., Mack, D., Dawson, D., Lawrence, E.,
            Willson, J.K.V., Lu, S., Nosrati, A., Swinier, S., Beard, L.,
            Lutterbaugh, J.D., Willis, J., Platzner, P., and Markowitz, S.
TITLE     Direct Submission
JOURNAL   Submitted (03-JUL-2002) Department of Medicine, Case Western
            Reserve University/Howard Hughes Medical Institute, 11001 Cedar
            Ave., Cleveland, OH 44106, USA
FEATURES  Location/Qualifiers
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICANT: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..921
OTHER INFORMATION: Clone 22 coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-091-952A-7

Query Match      26.7%; Score 352.2; DB 4; Length 921;
Best Local Similarity 73.1%; Pred. No. 4e-58;
Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

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DB 226 ACGGTGATGTGGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 285
QY 626 TTCTATCAGCCGACACCGAGGCGGAGGAGAGAGATGCTGCTGCTGCTGCTGCTGCTG 685
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DB 400 CCGCTCGGCCACCGAGCGCTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGCG 459
QY 806 CGCTTCAGGCCACCTATCGGTACTCTGACGACGAGATCGACTGCGCCACCCACCATCTCG 865
DB 460 CGCTTCAGGCCACCTATCGGTACTCTGACGACGAGATCGACTGCTCTCCACCATCTCC 519
QY 866 CTGTTCAGAGCGGAGAGGCCCCACCTACAGGGCCCTTGACCCCTTCAGCTTCGGGAC 925
DB 520 CTGTTCAGAGCGGAGAGGCCCCACCTACAGGGCCCTTGACCCCTTCAGCTTCGGGAC 579
QY 926 CCCGAGCAGAGCTGGAACTGAACCGGAGTTCGCTGCGCAGCCGCCCAACAGAACATC 985
DB 580 CTTGAAACAGAGATGGAACTGAACCGGAGTTCGCTGCGCAGCCGCCCAACAGAACATC 639
QY 986 TTCGACAGTGCATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 1042
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DB 700 AACTCGGGCATCAGTGCAGACACCTGCAGCAGTAACCGGAGGATGGAGGGGCCACCC 759
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RESULT 4
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; Sequence 6, Application US/09091952A
; Patent No. 6458532
; GENERAL INFORMATION:
; APPLICANT: Detera-Wadleigh, Sevilla D.
; Gershon, Elliot S.
; Badner, Judith A.
; Goldin, Lynn R.
; Berrettini, Wade H.
; Yoshikawa, Takeo
; Sanders, Alan R.
; Esterling, Lisa E.
; TITLE OF INVENTION: Chromosomal Markers and Diagnostic
; Tests for Manic-Depressive Illness
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 19-Apr-1999
; APPLICATION NUMBER: US/09/091,952A
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/029,278
; FILING DATE: 28-OCT-1996
; APPLICATION NUMBER: PCT/US97/19381
; FILING DATE: 28-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Timothy L.
; REGISTRATION NUMBER: 35,367
; REFERENCE/DOCKET NUMBER: 015280-297100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 6:
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; LOCATION: 1...8065
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; NAME/KEY: CDS
; LOCATION: 116...1036
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; NAME/KEY: misc feature
; LOCATION: 452...505
; OTHER INFORMATION: alternatively spliced portion
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; NAME/KEY: misc feature
; LOCATION: 5595...5685
; OTHER INFORMATION: amplified region for genotyping
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-091-952A-6

Query Match      26.7%; Score 352.2; DB 4; Length 8065;
Best Local Similarity 73.1%; Pred. No. 5.4e-58;
Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 506 CAGAGCATGGAGATCAGCGAGCTGGAGTTTCTCAGATCATCATCATCTGCTGGTGTGATG 565
DB 281 CCGGGCATCTTCAACTCGAGCTGGAGTTCCGCCAATCATCATCATCTGCTGGTGTGATG 340
QY 566 ATGGTGATGGTGGTGTGATCAGTGTCTGTGAGCCACTACAAAGCTGTCTGACGGTCC 625
DB 341 ACGGTGATGGTGGTGTGATCTGCTGTGCTGCTGAACCACTACAAAGTCTTCCACGGTCC 400
QY 626 TTCTATCAGCCGCGCAGACGAGCGGGGAGGAGAGATGCCCTGTCTCTCAGAGGATGC 685
DB 401 TTCTATCAGCCGCGCAGACGAGCGGGGAGGAGAGATGCCCTGTCTCTCAGAGGATGC 460
QY 686 CTGTGGCCCTCGGAGAGCACAGTGTCTAGGCAACGGAATCCAGAGCCGCGAGGTCTAGGCC 745
DB 461 CTGTGGCCCTCGGAGAGCACAGTGTCTAGGCAACGGAATCCAGAGCCGCGAGGTCTAGGCC 514
QY 746 CCGCTCGGCCACCGAGCGGCTGGCGTGGCGGCTTGGCCAGCGGAGCGGTCTCCAC 805
DB 515 GCCCGCGGTCAGGAGAGGTTCACAGCGGCTCTTTCATCCAGAGGATCGTTGAGC 574
QY 806 CGTTTCCAGCCACTATCCCTACTCTGACGACGAGATCGACCTGCCACCCACCATCTCG 865
DB 575 CGCTTCCAGCCACTATCCCTACTCTGACGACGAGATCGACCTGCCACCCACCATCTCG 634
QY 866 CTGTCTCAGCGGGAGGAGCGCCACCTTACGAGCGGCTTCCAGCTTCCAGCTTCCGAGC 925
DB 635 CTGTCTCAGCGGGAGGAGCGCCACCTTACGAGCGGCTTCCAGCTTCCAGCTTCCGAGC 694
QY 926 CCGGAGCAGCAGCTGGAAGTGAACCGGGAGTGGTGGCGGACACCCCAACAGAACCATC 985
DB 695 CCGGAGCAGCAGCTGGAAGTGAACCGGGAGTGGTGGCGGACACCCCAACAGAACCATC 754
QY 986 TTCGACAGTACCTGATGATGATGTCAGG---CTGGCGGCGGCTTCCAGCTTCCGAGT 1042
DB 755 TTCGACAGTACCTGATGATGATGTCAGG---CTGGCGGCGGCTTCCAGCTTCCGAGT 814
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DB 815 AACTCGGCGATCAGTGCAAGCACCTGTCAGCAGTAAAGGAGGATGGAGGGCCACCCGCC 874
QY 1103 ACCTCAGCGAGTATCGGCGACTACCGGGGTCTCTTCCAGCAGCAGCAGAGCAG 1161
DB 875 ACATCAGCGAGTATGGGCGACCAACCGAGCGGCTTCTTCTCCATCCACGAGCGAG 933

RESULT 5
US-09-091-952A-8
; Sequence 8, Application US/09091952A
; Patent No. 6458532
; GENERAL INFORMATION:
; APPLICANT: Deters-Wadleigh, Sevilla D.
; Gershon, Elliot S.
; Badner, Judith A.
; Goldin, Lynn R.
; Berrettini, Wade H.
; Yoshikawa, Takeo
; Sanders, Alan R.
; Esterling, Lisa E.
; TITLE OF INVENTION: Chromosomal Markers and Diagnostic

; NUMBER OF SEQUENCES: 197
; Tests for Manic-Depressive Illness
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1...867
OTHER INFORMATION: Clone 22 isoform 2 alternatively
spliced coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-091-952A-8

Query Match      21.5%; Score 284.2; DB 4; Length 867;
Best Local Similarity 68.7%; Pred. No. 2.7e-45;
Matches 453; Conservative 0; Mismatches 143; Indels 63; Gaps 2;

QY 506 CAGAGCATGGAGATCAGCGAGCTGGAGTTTGTTCAGATCATCATCATCTGCTGGTGTGATG 565
DB 166 CCGGGCATCTTCAACTCGGAGCTGGAGTTTCCGCCAATCATCATCATCTGCTGGTGTGATG 225
QY 566 ATGGTGATGGTGGTGTGATCAGTGTCTGTGAGCCACTACAAAGCTGTCTGACGGTCC 625
DB 226 ACGGTGATGGTGGTGTGATCTGCTGTGCTGCTGAACCACTACAAAGTCTTCCACGGGTC 285
QY 626 TTCTATCAGCGCGCAGACGAGCGGGGAGGAGAGATGCCCTGTCTCTCAGAGGATGC 685
DB 286 TTCTATCAGCGCGCGCAGACGAGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 329
QY 686 CTGTGGCCCTCGGAGAGCAGTGTCTCAGGCAACGGAATCCAGAGCGGCGAGGCTTACGGC 745
DB 330 -----GCCGCGAGATCATGAT 345
QY 746 CCGCCCTCGGCCACGAGCGGCTGGCGGCTTCCGCCAGCGGAGGAGGAGGAGGAGGAGGAGGAGG 805
DB 346 GCCCGCGGTCAGGAGCAGGTTTACAGCGCGCTTCTTCTCAGAGGAGTGGTTCAGC 405
QY 806 CGTTTCCAGCCACTATCCCTACTCTGACGACGAGATCGACCTGCCACCCACCATCTCG 865
DB 406 CGCTTCCAGCCACTATCCCTACTCTGACGACGAGATCGACCTGCCACCCACCATCTCG 465
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QY 866 CTGTACAGCGGAGGAGCCGCCACCTACAGCGCCCTGACACCTTCAGCTTCGGGAC 925
Db |||||
QY 466 CTGTCCGACGCTGAGAGACCACTCTTACAGGGCCCTGACCTCTGAGCTTCGGGAC 525
Db |||||
QY 926 CCGGAGCAGAGCTGGAACCGGAGATCGGTGCGGCAACCCCAAGAACATC 985
Db |||||
QY 526 CCTGAACAGCAGATGGAACCTCAACCGAGAGTCCGTGAGGGCCCAACCAACCAAT 585
QY 986 TTGACAGTACCTGATGGATAGTCCAGG--CTGGGGCGCCCTGCCCCCCAGCAGT 1042
Db |||||
QY 586 TTTGACAGTATTTAATAGACATGCTATGTATAGGGGGTTCATGCCCAACCAAGC 645
QY 1043 AACTCGGGCATACGCCACCTGCTACGGCAGCGGGCGGCATGAGGGCGCGCCGCC 1102
Db |||||
QY 646 AACTCGGGCATACGTCAGCAAGCCTGAGCAGTAAACGGAGGATGAGGGGCCACCC 705
QY 1103 ACCTACAGCAGTCACTCGGCCACTACCGGGGTCTCTTCCAGCAGCAGCAGAG 1161
Db |||||
QY 706 ACATACAGGAGGTGATGGGCCACCAACCGAGCGCTCTTTCTTCATCAGCAGCAG 764

RESULT 6

US-09-621-976-2162
; Sequence 2162, Application US/09621976
; Patent No. 8639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PE2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2162
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 17..223
US-09-621-976-2162

Query Match 6.8%; Score 90.4; DB 4; Length 391;
Best Local Similarity 75.7%; Pred. No. 8.6e-09;
Matches 112; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 1019 GGCGGCCCCCTGCCCCCAGCAGTAACCTCGGGCATCAGCCACGTCGTCACGCGCGGC 1078
Db GGGGGTCCATGCCCCCAGCAGCACTCGGGCATCAGTCAAGCACCTGACGAGTAAC 85
QY 1079 GGGCGCATGGAGGGCGCCGCCACCTACAGCAGGTCTCGGCCACTACCGGGGTCC 1138
Db GGGAGGATGGAGGGCGCCGCCACATACAGCAGGTGATGGGCCACCCAGCGGCC 145
QY 1139 TCCTTCCAGCAGCAGCAGCAGTGGGC 1166
Db |||||
QY 146 TCTTCTCCATCACCAGCGCAGAACGC 173
Db |||||

RESULT 7

US-09-616-289-48/c
; Sequence 48, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 2561
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (246)...(1895)
US-09-616-289-48

Query Match 5.7%; Score 75.4; DB 4; Length 2561;
Best Local Similarity 53.0%; Pred. No. 7.6e-06;
Matches 206; Conservative 0; Mismatches 181; Indels 2; Gaps 2;
QY 56 GCGCGCGCGCGCGCGCGCGCGCTCGGCTGGGGAAGCTAGCGGAGAGGCTCA 115
Db 875 GCG 816
QY 116 GCCCGCGCGCGCGCGCGCGCGCGCTGCCACGCCATTTTCGGAGCGCCACCGCGGCGAC 175
Db 815 CGGGGGAGCG 756
QY 176 TGCCGACGCCCGCGCGCGCTGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCG 235
Db 755 GCCCGGCTGCG 697
QY 236 CGCACTGAGCG 295
Db 696 CGCGGGCG 637
QY 296 CGCGCTCCCCCGCGCGCGCTCTCTGATCGCGCGCGCGCGCGCGCGCGCGCGCG 355
Db 636 CGGGGTGCG 578
QY 356 GCG 415
Db 577 GCG 518
QY 416 CACCGCTTGATGGGGGTCAACAGCACCGC 444
Db 517 CTCCTTGTAGTGAACCGGAGCAGCGC 489

RESULT 8

US-09-616-289-48
; Sequence 48, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02

;; PRIOR APPLICATION NUMBER: US 08/979,608
;; PRIOR FILING DATE: 1997-11-26
;; PRIOR APPLICATION NUMBER: US 60/031,930
;; PRIOR FILING DATE: 1996-11-27
;; PRIOR APPLICATION NUMBER: US 60/048,547
;; PRIOR FILING DATE: 1997-06-03
;; NUMBER OF SEQ ID NOS: 53
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 48
;; LENGTH: 2561
;; TYPE: DNA
;; ORGANISM: Oryctolagus cuniculus
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (246)...(1895)
US-09-616-289-48

Query Match 5.5%; Score 72.2; DB 4; Length 2561;
Best Local Similarity 51.1%; Pred. No. 3.1e-05;
Matches 170; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

QY 133 CGCCCGCTGTCAGAGCCATTTCCGAGACGCCACCCGCGGGGCACTGCCAGACCCCGGGG 192
Db 528 CGCAACGCGCGCGCTCCAGCGCCCGCGCGCGAGCCACCCCGCGCGCCCGCGCGCG 587
QY 193 CTGCGAGAGGAGCGCGGGGGCGGAGCGAGCGCGTCCCGCGCACTGAGCCCGCGG 252
Db 588 GCCCGCGCGGGGCG 647
QY 253 CGCCCGCGGAACTTGGCGGCGACCGAGACCCCGCGAGCGGGCGCGCTCCCGCGCG 312
Db 648 CGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 707
QY 313 GGGCTCTGTCATGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 372
Db 708 GCGCTGCGCGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 767
QY 373 CGAGCG 432
Db 768 CGGGCG 827
QY 433 CAACAGCAGCG 465
Db 828 CG 860

RESULT 9
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Query Match 5.3%; Score 70.4; DB 3; Length 4403765;

Best Local Similarity 50.0%; Pred. No. 0.0002;
Matches 230; Conservative 0; Mismatches 226; Indels 4; Gaps 2;

QY 2 GACCGCGGCTCGAGCGCAACCCCGATCTCTTGGACTTGAATGAGGAGGAGCGCGC 61
Db 3936335 GCGCGCGGCAACCGCGCGCACCGCGCGCAGAGGCGGAGTGTGCGCGCGCGCGCG 3936394
QY 62 GCGCGCGCGCGCGCGCGCGCGCTCGGTGGGGAAGCTAGCGGCGAGAGCTCAGCCCCG 121
Db 3936395 ATCGGTGGGTCTCGCGCGCGCAAGGCGCGCAACCGCGCGGACCGCAAGTCCGCGGTGCG 3936454
QY 122 GCGGAGCGCGCGCGCGCGCGCTGCCAGCGCCATTTTCGGAGCGCACCCCGCGGCACTCCCG 180
Db 3936455 GCGGCG 3936514
QY 181 -ACGCCCCCGCGGCTCGCGAGGAGCGCGGGGGCGCGAGCGCGGCGCGCGCGCGCGCG 239
Db 3936515 CAAGGCGCGAGCGGTGTGCGGTGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3936574
QY 240 CTGAGCGCGCGCGCGCGCGCGCGCGGGAATTTGGCGGCGACCCCGCGAGCGCGGCGCG 299
Db 3936575 AACGCGACCGCTGGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3936634
QY 300 CTCTCCCGCGCGCGCGCGCTCTCTGATGCGGGGCGCGCGCGCGCGCGCGCGCGCGCG 359
Db 3936635 GCCTCTCTAGCTACCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3936692
QY 360 CCG 419
Db 3936693 GCAGCG 3936752
QY 420 GCTTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 459
Db 3936753 GCGGACAGGTGCG 3936792

RESULT 10
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 5.2%; Score 68.8; DB 3; Length 4411529;
Best Local Similarity 49.8%; Pred. No. 0.00039;
Matches 229; Conservative 0; Mismatches 227; Indels 4; Gaps 2;

QY 2 GACCGCGGCTCGAGCGCAACCCCGATCTCTTGGACTTGAATGAGGAGGAGCGCGC 61
Db 3942788 GCGCGCGGCAACCGCGCGCACCGCGCGCAGAGCGCGGCGAGTGTGCGCGCGCGCGCG 3942847
QY 62 GCGCGCGCGCGCGCGCGCGCGCTCGGTGGGGAAGCTAGCGGCGAGAGCTCAGCCCCG 121
Db 3942848 ATCGGTGGGTCTCGCGCGCGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 3942907
QY 122 GCGGAGCGCGCGCGCGCGCGCTGCCAGCCATTTTCGGAGCGCACCCCGCGGCACTCCCG 180

NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 350..14002
FEATURE:
NAME/KEY: CDS
LOCATION: 14046..20036
FEATURE:
NAME/KEY: CDS
LOCATION: 20110..31284
FEATURE:
NAME/KEY: CDS
LOCATION: 31329..36071
FEATURE:
NAME/KEY: CDS
LOCATION: 36155..41830
US-08-804-198-1

Query Match 5.1%; Score 68; DB 2; Length 44377;
Best Local Similarity 49.2%; Pred. No. 0.00029;
Matches 234; Conservative 0; Mismatches 240; Indels 2; Gaps 2;

QY 5 CCGCGTCTCGAGCGAAACCCGATCTCTTGGACTTGAATGAGGAGGAGGCGGCGGC 64
Db 19499 CTCGGGTGCGGAACCTCCGCGAGCGCGCCAGCTCCGCGGGGTGCGCGGGC 19440

QY 65 GCGCGGCGGCGGAGCGCTCGGTGGGAAAGTACGCGAGAGGCTCAGCCCGCGG 124
Db 19439 GGGGCGAGGCGCACGCGACCGTCTCTGTCGCGGTGCTCCCGCGCGCGCGTCT 19380

QY 125 GCAGCGCGCGCGCGCGCTGCGAGCCATTTTCGAGCGCCACCCCGCGGCACTGCGGACG 184
Db 19379 GCGGCGCTCGCGGTACGCGCGCCAGGTACGCGAGGACCTCCCGGAGAGCGTGGCACC 19320

QY 185 CCGCGGCGCTCGGAGGAGCGCGGCGGCGGCGAGCGGCTCCCGCGACTGAG 244
Db 19319 GCGCGCGCGCGCGAGTCCAGCGCGACGCGGCGAGCGCGCTCGGCGCGGT-CAGCG 19261

QY 245 CCGCGCGCGCGCGCGCGAACTTGGCGGCGACCCCGAGCGCGCGCGCGCGCGCTCC 304
Db 19260 CCGGTGCGAGGAGTCCAGTCCGCGCGCGCGGTTCGAGCGGCGCGAGACCGAGCGCTGA 19201

QY 305 CCGCGCGCGCGCTCTGATCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 364
Db 19200 CCGCGCGCGCGCTCTGATCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19141

QY 365 GCG 424
Db 19140 AGCCGAGCGAGCGCGGCTCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19082

QY 425 ATGGGGTCAACAGCAGCG 480
Db 19081 AAGGGTTGGCGCGCGCGTACCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCG 19026

RESULT 13

US-08-690-473-1/c
Sequence 1, Application US/08690473
Patent No. 5876923
GENERAL INFORMATION:
APPLICANT: Leopardi, Rosario
APPLICANT: Roizman, Bernard

TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 AS AN
INHIBITOR OF APOPTOSIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,473
FILING DATE: 26-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-690-473-1

Query Match 5.1%; Score 67.6; DB 2; Length 4257;
Best Local Similarity 48.8%; Pred. No. 0.00024;
Matches 239; Conservative 0; Mismatches 249; Indels 2; Gaps 2;

QY 40 TGAATGAGAGGAGGAGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 99
Db 2828 TGCTGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2769

QY 100 TAGCGGACAGAGGTCTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 159
Db 2768 CGCGCGGACACG 2709

QY 160 CGCCACCGCGCGGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 219
Db 2708 GGTGCGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2649

QY 220 GCGGAGCGCGGTCCGCGCGCACTGAGCC-CGCGCGCGCGCGCGCGCGCGCGCGCG 278
Db 2648 GGGCGCGCGGTCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2589

QY 279 AGCCCG 338
Db 2588 GGGCG 2529

QY 339 TCGG-GGCG 397
Db 2528 GGGCGCGCGAGCG 2469

QY 398 GCGCGCGCGCGTCCATGACCGCTTGATGGGGGTCAACAGCAGCGCGCGCGCGCGCG 457
Db 2468 GCGCGCGAGGCG 2409

QY 458 GGGCAGCGCAATGTCTCTGCGAGGTGCACTCAACCGCTCTTGTTCAGAGCATGGAG 517
Db 2408 GCGGAGCTCGGCGAGCGCGCGGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2349

QY 518 ATCAGCGGAGC 527
Db 2348 CTCAGCGGCGC 2339

us-09-934-249-1.rni

Thu May 13 08:29:17 2004

Search completed: May 12, 2004, 05:21:48
Job time : 152.422 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2004, 03:27:13 ; Search time 639.311 Seconds
(without alignments)
9360.266 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321

Sequence: 1 CGACCGGGTCTCGGAGCGA.....CTGCGTAGGTGAAGGCGAG 1321

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA..*

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- 10: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1321	100.0	1321	9	US-09-934-249-1
2	1229	93.0	4839	15	US-10-241-220-119
3	1229	93.0	4839	15	US-10-269-909-84
4	1229	93.0	4839	15	US-10-269-909-85
5	864	65.4	864	16	US-10-295-027-127
6	861	65.2	861	9	US-09-934-249-3
7	803.2	60.8	969	10	US-09-796-753-55
8	802.2	60.7	1141	15	US-10-205-823-412
9	802.2	60.7	1141	15	US-10-301-822-208
10	802.2	60.7	1850	15	US-10-241-220-44
11	802.2	60.7	4527	10	US-09-821-812-2
12	801.6	60.7	1140	15	US-10-390-045-1
13	790.4	59.8	1066	14	US-10-098-841-71
14	767.4	58.1	806	15	US-10-241-220-45

15	755.8	57.2	759	15	US-10-390-045-2	Sequence 12, Appli
16	616.4	46.7	878	9	US-09-934-249-12	Sequence 12, Appli
17	589.2	44.6	1583	15	US-10-000-256A-32	Sequence 32, Appl
18	493.6	37.4	693	9	US-09-934-249-14	Sequence 14, Appl
19	466.2	35.3	1713	10	US-09-796-753-57	Sequence 57, Appl
20	352.2	26.7	921	15	US-10-251-598-7	Sequence 0, Appli
21	352.2	26.7	8018	13	US-10-087-192-1667	Sequence 0, Appli
22	352.2	26.7	8065	15	US-10-251-598-6	Sequence 0, Appli
23	350	26.5	920	13	US-09-823-245A-20	Sequence 20, Appl
24	350	26.5	2170	16	US-10-094-749-137	Sequence 197, App
25	349	26.4	8093	9	US-09-934-249-16	Sequence 16, Appl
26	349	26.4	8093	13	US-10-343-887-1023	Sequence 1023, Ap
27	349	26.4	8093	13	US-10-172-118-1023	Sequence 1023, Ap
28	341.8	25.9	475	9	US-09-934-249-15	Sequence 15, Appl
29	284.2	21.5	867	15	US-10-251-598-8	Sequence 0, Appli
30	250.2	18.9	285020	13	US-10-087-192-1666	Sequence 1666, Ap
31	182	13.8	368	9	US-09-783-590-3464	Sequence 3464, Ap
32	182	13.8	467	10	US-09-918-995-2074	Sequence 2074, Ap
33	100.2	7.6	522	13	US-10-240-425-166	Sequence 166, App
34	79.6	6.0	51657	16	US-10-057-475B-10475	Sequence 10475, A
35	79.6	6.0	51657	16	US-10-154-884B-10475	Sequence 10475, A
36	78	5.9	4020	10	US-09-796-679-5	Sequence 5, Appli
37	77.6	5.9	606	13	US-10-424-593-95310	Sequence 95310, A
38	75.4	5.7	2581	9	US-09-976-740-48	Sequence 48, Appl
39	75.4	5.7	2561	13	US-10-671-242-48	Sequence 48, Appl
40	75.4	5.7	2561	14	US-10-023-523-48	Sequence 48, Appl
41	75.4	5.7	2561	14	US-10-023-523-48	Sequence 48, Appl
42	75.4	5.7	2561	16	US-10-616-187-48	Sequence 48, Appl
43	72.2	5.5	2307	10	US-09-893-519A-87	Sequence 87, Appl
44	72.2	5.5	2561	9	US-09-976-740-48	Sequence 48, Appl
45	72.2	5.5	2561	13	US-10-671-242-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1

US-09-934-249-1
; Sequence 1, Application US/09934249
; Patent No. US20020115081A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Richard T.
; APPLICANT: Landschulz, Katherine T.
; APPLICANT: Turi, Thomas G.
; APPLICANT: Thompson, John F.
; APPLICANT: Kennedy, Scott P.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
; FILE REFERENCE: P0738/7001/ERP/KA
; CURRENT APPLICATION NUMBER: US/09/934,249
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,159
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (413) ... (1273)
US-09-934-249-1

Query Match 100.0%; Score 1321; DB 9; Length 1321;

Best Local Similarity 100.0%; Pred. No. 5.3e-293;

Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACCGGGTCTCGGAGCGAACCAGATCTCTTGGACTTGAATGAGGAGGAGCGG 60

Db 1 CGACCGGGTCTCGGAGCGAACCAGATCTCTTGGACTTGAATGAGGAGGAGCGG 60

QY 61 CGGCGGGCGGCGGCGGCGGCTCGCTCGGGGAAGACTAGCGGAGAGCTCAGCCCC 120

901	GTGACCTGATGGATAGTGCAGCTGGCGCGCCCTGCCCCCAGCAGTAATCTGGGCA	960
1053	TCAGCGCCACGTGCTTACGCAAGGGCGGCGCATGAGAGGGCGCGCCCACTACAGCG	1112
961	TCAGCGCCACGTGCTTACGCAAGGGCGGCGCATGAGAGGGCGCGCGCCCACTACAGCG	1020
1113	AGGTCATCGGCCACTACCCGGGGTCTCTCTTCAGCACCCAGCAGACGACGTGGGCCGCCCT	1172
1021	AGGTCATCGGCCACTACCCGGGGTCTCTCTTCAGCACCCAGCAGACGACGTGGGCCGCCCT	1080
1173	CTTGTCTGAGGGAGCCGGCTCCACACACACACATCGCGCCCTTAGAGAGCGCAGCCA	1232
1081	CTTGTCTGAGGGAGCCGGCTCCACACACACACATCGCGCCCTTAGAGAGCGCAGCCA	1140
1233	TCGTGGAGCAAGAGAGAGGATAACAGAAAGGACACCCCTCTCTAGGGTCCCAGGGGGGCC	1292
1141	TCGTGGAGCAAGAGAGAGGATAACAGAAAGGACACCCCTCTCTAGGGTCCCAGGGGGGCC	1200
1293	GGGCTGGGCTGCGTAGGTGAAAAGGCAG	1321
1201	GGGCTGGGCTGCGTAGGTGAAAAGGCAG	1229

RESULT 4

```

US-10-269-909-85
; Sequence 85, Application US/10369909
; Publication No. US20030180747A1
; GENERAL INFORMATION:
; APPLICANT: HRUBAN, RALPH H.
; APPLICANT: ARGANI, PEDRAM
; APPLICANT: TACOBUZIO-DONAHUE, CHRISTINE
; APPLICANT: MAITRA, ANIRBAN
; TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES
; FILE REFERENCE: 58303(71699)
; CURRENT APPLICATION NUMBER: US/10/269,909
; CURRENT FILING DATE: 2003-10-11
; PRIOR APPLICATION NUMBER: 60/328,609
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/332,754
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 85
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-269-909-85

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Query Match	93.0%; Score 1229; DB 15; Length 4839;
Best Local Similarity	100.0%; Pred. NO. 6.3e-272;
Matches 1229; Conservative	0; Mismatches 0; Gaps 0;
QY	93 GGAAGCTACGGCAGAGGCTCAGCCCGCGCGCAGCGCGCGCCCTGCCAGCCCATTT 152
Db	1 GGAAGCTACGGCAGAGGCTCAGCCCGCGCGCAGCGCGCCCTGCCAGCCCATTT 60
QY	153 TTCGGAGCGACCCCGGGGCACTGCCGAGCGCCCCCGGGCTGCCGAGGGAGCGCGGG 212
Db	61 TTCGGAGCGACCCCGGGGCACTGCCGAGCGCCCCCGGGCTGCCGAGGGAGCGCGGG 120
QY	213 GGGCGCAGCGAGCGCGGTCCCGCGCACTAGCCCCCGCGCGCCCCGGGAACTTGGCGGC 272
Db	121 GGGCGCAGCGAGCGCGGTCCCGCGCACTAGCCCCCGCGCGCCCCGGGAACTTGGCGGC 180
QY	273 GACCCGAGCCCGGAGCGCGGGCGCGCTTCCCCCGCGCGCGGCTCTTCATGCGGGGGC 332
Db	181 GACCCGAGCCCGGAGCGGGGCGCGCTTCCCCCGCGCGCGGCTCTTCGATGCGGGGC 240
QY	333 CCCAGCTTCGGGGCGCCCGGCGCGAGCCCCCCCCCGGCGCGCCCCCGGCGCCCCGC 392
Db	241 CCCAGCTTCGGGGCGCGCGCGAGCCCCCCCCCGGCGCGCCCCCGGAGCCCCCGGCGCCGC 300

RESULT 5

US-10-295-027-127
; Sequence 127, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Azi, Natasha
; APPLICANT: Ginsberg, Wendy M.

APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MEM01-029P2RNK
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 208
LENGTH: 1141
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (96)...(854)
US-10-301-822-208

Query Match 60.7%; Score 802.2; DB 15; Length 1141;
Best Local Similarity 98.4%; Pred. No. 3e-174; Indels 0; Gaps 0;
Matches 810; Conservative 0; Mismatches 13

QY 499 TTGTTCAGAGCATGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCTGCTGT 558
DB 77 TCTCTCGCAACAGGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCTGCTGT 136

QY 559 GGTGATGATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 618
DB 137 GGTGATGATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 196

QY 619 ACGGTCTTCATCAGCCGGCAGCCAGGCGGGGAGAGAGATGCCCTGTCTCAGA 678
DB 197 ACGGTCTTCATCAGCCGGCAGCCAGGCGGGGAGAGAGATGCCCTGTCTCAGA 256

QY 679 AGGATGCTGTGGCCCTCGGAGACAGTGTGAGCAACCGAATCCAGAGCCGAGGT 738
DB 257 AGGATGCTGTGGCCCTCGGAGACAGTGTGAGCAACCGAATCCAGAGCCGAGGT 316

QY 739 CTTACCGCTTCAGCCCGCAGCTGTAACCGGAGTGTGTCGCGGACCCCAACAG 918
DB 437 CTTACCGCTTCAGCCCGCAGCTGTAACCGGAGTGTGTCGCGGACCCCAACAG 978

QY 919 TCGGAGCCCGCAGCAGCTGTAACCGGAGTGTGTCGCGGACCCCAACAG 978
DB 497 TCGGAGCCCGCAGCAGCTGTAACCGGAGTGTGTCGCGGACCCCAACAG 556

QY 979 AACCATCTTCGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1038
DB 557 AACCATCTTCGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 616

QY 1039 CAGTAACCTCGGCATCAGCCGACGTCGTACCGGAGCGGCGGCATGAGAGGGCGCC 1098

DB 617 CAGTAACCTCGGCATCAGCCGACGTCGTACGGCAGCGCGGCATGAGAGGGCGCC 676
QY 1099 GCCCACCCTACAGCAGGTCATCGGCCACTACCCGGGGTCTCTCTCCAGCACCAGCAG 1158
DB 677 GCCCACCCTACAGCAGGTCATCGGCCACTACCCGGGGTCTCTCTCCAGCACCAGCAG 736
QY 1159 CAGTGGCGCCCT 1218
DB 737 CAGTGGCGCCCT 796
QY 1219 AGAGAGCGCAGCATCTGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1278
DB 797 AGAGAGCGCAGCATCTGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 856
QY 1279 TCCCGAGGGGGCGCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 1321
DB 857 TCCCGAGGGGGCGCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 899

RESULT 10
US-10-241-220-44
Sequence 44, Application US/10241220
Publication No. US20030148408A1
GENERAL INFORMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Mickey
APPLICANT: Wu, Thomas
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 44
LENGTH: 1850
TYPE: DNA
ORGANISM: Homo Sapien
US-10-241-220-44

Query Match 60.7%; Score 802.2; DB 15; Length 1850;
Best Local Similarity 98.4%; Pred. No. 3.1e-174; Indels 0; Gaps 0;
Matches 810; Conservative 0; Mismatches 13

QY 499 TTGTTCAGAGCATGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCTGCTGT 558
DB 77 TCTCTCGCAACAGGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCTGCTGT 136

QY 559 GGTGATGATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 618
DB 137 GGTGATGATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 196

QY 619 ACGGTCTTCATCAGCCGGCAGCCAGGCGGGGAGAGAGATGCCCTGTCTCAGA 678
DB 197 ACGGTCTTCATCAGCCGGCAGCCAGGCGGGGAGAGAGATGCCCTGTCTCAGA 256

QY 679 AGGATGCTGTGGCCCTCGGAGACAGTGTGAGCAACCGAATCCAGAGCCGAGGT 738
DB 257 AGGATGCTGTGGCCCTCGGAGACAGTGTGAGCAACCGAATCCAGAGCCGAGGT 316

QY 739 CTTACCGCTTCAGCCCGCAGCTGTAACCGGAGTGTGTCGCGGACCCCAACAG 918
DB 437 CTTACCGCTTCAGCCCGCAGCTGTAACCGGAGTGTGTCGCGGACCCCAACAG 978

QY 919 TCGGAGCCCGCAGCAGCTGTAACCGGAGTGTGTCGCGGACCCCAACAG 978
DB 497 TCGGAGCCCGCAGCAGCTGTAACCGGAGTGTGTCGCGGACCCCAACAG 556

QY 979 AACCATCTTCGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1038
DB 557 AACCATCTTCGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 616

QY 1039 CAGTAACCTCGGCATCAGCCGACGTCGTACCGGAGCGGCGGCATGAGAGGGCGCC 918

Db 653 CGTGTACGGCAGCGCGGGCGCATGGAGGGCGCGCGCCACCTACAGCGAGTATCG 712
 QY 1122 GCCACTACCCGGGGTCTCTTCCAGCACAGCAGAGTGGCGCGCCCTCTCTTGGTGG 1181
 Db 713 GCCACTACCCGGGGTCTCTTCCAGCACAGCAGAGTGGCGCGCCCTCTTGGTGG 772
 QY 1182 AGGGGACCCGGTCTCCACACACACATCGCGCCCTAGAGAGCGAGCATCTGGAGCA 1241
 Db 773 AGGGGACCCGGTCTCCACACACACATCGCGCCCTAGAGAGCGAGCATCTGGAGCA 832
 QY 1242 AAGAGAAGGATAAACAAGAGGACACCTCTCTAGGGTCCCCAGGGGGCGCGGGTGGGG 1301
 Db 833 AAGAGAAGGATAAACAAGAGGACACCTCTCTAGGGTCCCCAGGGGGCGCGGGTGGGG 892
 QY 1302 CTCGGTAGGTGAAAAGGCAG 1321
 Db 893 CTCGGTAGGTGAAAAGGCAG 912

RESULT 14

US-10-241-220-45
 ; Sequence 45, Application US/10241220
 ; Publication No. US20030148408A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Frantz, Gretchen
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Phillips, Heidi
 ; APPLICANT: Polakis, Paul
 ; APPLICANT: Spencer, Susan
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wu, Thomas
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
 ; TREATMENT OF TUMOR
 ; FILE REFERENCE: P501091-US
 ; CURRENT APPLICATION NUMBER: US/10/241,220
 ; CURRENT FILING DATE: 2002-12-13
 ; NUMBER OF SEQ ID NOS: 120
 ; SEQ ID NO 45
 ; LENGTH: 806
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-241-220-45

Query Match 58.1%; Score 767.4; DB 15; Length 806;
 Best Local Similarity 98.0%; Pred. No. 2.8e-166;
 Matches 777; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 499 TTGTTCCAGCATGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCATCGTGT 558
 Db 14 TCTCCTCGAAACAGGCAATGGCGAGCTGGAGTTGTTTCAGATCATCATCATCGTGT 73
 QY 559 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 618
 Db 74 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 133
 QY 619 ACGGTCTTTCATGACCGCGCACAGCCAGGGGGCGGAGAGAGATGCCCTGTCCTAGA 678
 Db 134 ACGGTCTTTCATGACCGCGCACAGCCAGGGGGCGGAGAGAGATGCCCTGTCCTAGA 193
 QY 679 AGGATGCTGTGGCCCTCGAGAGACAGATGTCAGGCAACGGATCCAGAGCGCGAGGT 738
 Db 194 AGGATGCTGTGGCCCTCGAGAGACAGATGTCAGGCAACGGATCCAGAGCGCGAGGT 253
 QY 739 CTACGCCCCGGCTCGGCCCAACCGACCGCTGGCGGTGGCGCCCTTGGCCCGAGCGGAGCG 798
 Db 254 CTACGCCCCGGCTCGGCCCAACCGACCGCTGGCGGTGGCGCCCTTGGCCCGAGCGGAGCG 313
 QY 799 CTTCCACCGCTTCAGCGCCACCTATCGTACCTGTCAGCAGAGATGACCTGCCACCCAC 858
 Db 314 CTTCCACCGCTTCAGCGCCACCTATCGTACCTGTCAGCAGAGATGACCTGCCACCCAC 373
 QY 859 CATCTCGTGTGACAGCGGGAGGAGCCCCACCCCTACAGGGGCCCTGACCCCTCCAGCT 918

Db 374 CATCTCGTGTGACAGCGGGAGGAGCCCCACCTACCGGGGCCCTTCACCTCCAGCT 433
 QY 919 TCGGGACCCCGAGCAGAGCTGGAACTGAACCGGGAGTGGTGGCGCGCACCCCCAAACAG 978
 Db 434 TCGGGACCCCGAGCAGAGCTGGAACTGAACCGGGAGTGGTGGCGCGCACCCCCAAACAG 493
 QY 979 AACCATCTTGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1038
 Db 494 AACCATCTTGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 553
 QY 1039 CAGTAACTCGGGCATCAGCGCCAGTGTCTACGGCAGCGGGCGGCGCATGAGGGGGCGGCC 1098
 Db 554 CAGTAACTCGGGCATCAGCGCCAGTGTCTACGGCAGCGGGCGGCGCATGAGGGGGCGGCC 613
 QY 1099 GCCCAGCTACAGCAGAGTCACTACCGCGGCTCTCTTTCAGCAGACACAGCAGAG 1158
 Db 614 GCCCAGCTACAGCAGAGTCACTACCGCGGCTCTCTTTCAGCAGACACAGCAGAG 673
 QY 1159 CAGTGGGCGGCCCTCTCTTGTGGAGGGAGCCCGGCTCCACACACACACATCGCGCCCT 1218
 Db 674 CAGTGGGCGGCCCTCTCTTGTGGAGGGAGCCCGGCTCCACACACACACATCGCGCCCT 733
 QY 1219 AGAGAGCGCAGCCATCTGGAGCAAGAGAGGATAAAGAGAGGACACCCCTCTCTAGGG 1278
 Db 734 AGAGAGCGCAGCCATCTGGAGCAAGAGAGGATAAAGAGAGGACACCCCTCTCTAGGG 793
 QY 1279 TCCCCAGGGGGC 1291
 Db 794 TCCCCAGGAAGGC 806

RESULT 15

US-10-390-045-2
 ; Sequence 2, Application US/10390045
 ; Publication No. US20030170713A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SRIVASTAVA, SHIV
 ; APPLICANT: MOUL, JUDD W.
 ; APPLICANT: XU, LINDA L.
 ; APPLICANT: SEGAWA, TAKEHIKO
 ; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
 ; FILE REFERENCE: 04995.0057-00000
 ; CURRENT APPLICATION NUMBER: US/10/390,045
 ; CURRENT FILING DATE: 2003-03-18
 ; PRIOR APPLICATION NUMBER: US/09/769,482
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 60/178,772
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: 60/179,045
 ; PRIOR FILING DATE: 2000-01-31
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 759
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-390-045-2

Query Match 57.2%; Score 755.8; DB 15; Length 759;
 Best Local Similarity 99.7%; Pred. No. 1.3e-163;
 Matches 757; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 518 ATCAGGAGCTGGAGATTTGTTTCAGATCATCATCATCATCATCATCATCATCATCAT 577
 Db 1 ATGCGGAGCTGGAGTTTGTTCAGATCATCATCATCATCATCATCATCATCATCAT 60
 QY 578 GTGGTGAATCAGCTGCTGCTGAGCCACTACAGCTGTCTGACCGGTCTCTTCATCAGCCGG 637
 Db 61 GTGGTGAATCAGCTGCTGCTGAGCCACTACAGCTGTCTGACCGGTCTCTTCATCAGCCGG 120
 QY 638 CACAGCCAGGGGGCGGAGGAGAGATGCTCTGCTCTCAGAGAGATGCTGTGGCCCTCG 697

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Db 121 CACAGCCAGGCGCGAGAGAGAGATGCCCTGTCTCAGAGGATGCTGTGCCCCCTCG 180
QY 698 GAGAGCAAGTGTACGGCAACGGAAATCCAGAGCGCAGGTCTACGCCGCCCTCGCCCC 757
Db 181 GAGAGCAAGTGTACGGCAACGGAAATCCAGAGCGCAGGTCTACGCCGCCCTCGCCCC 240
QY 758 ACCGACCGCTGGCGCTGCGCCCTTCGCCCCAGAGGGAGCGCTTCCACCGCTTCCAGCCC 817
Db 241 ACCGACCGCTGGCGCTGCGCCCTTCGCCCCAGAGGGAGCGCTTCCACCGCTTCCAGCCC 300
QY 818 ACCTATCCGTACCTCCAGCAGAGATCGACCTGCGCACCCACCATCTCGCTCTCAGACGGG 877
Db 301 ACCTATCCGTACCTCCAGCAGAGATCGACCTGCGCACCCACCATCTCGCTCTCAGACGGG 360
QY 878 GAGGAGCCCCCACCCTTACAGGGCCCCCTGCACCTTCCAGCTTCGGGACCCCGAGCAGAG 937
Db 361 GAGGAGCCCCCACCCTTACAGGGCCCCCTGCACCTTCCAGCTTCGGGACCCCGAGCAGAG 420
QY 938 CTGGAACCTGAACCGGGAGTGGTGGCGCACCCCCCAACAGAACCATCTTCGACAGTGAC 997
Db 421 CTGGAACCTGAACCGGGAGTGGTGGCGCACCCCCCAACAGAACCATCTTCGACAGTGAC 480
QY 998 CTGATGGATAGTGCAGGCTGGCGCGCCCTGCCCCCAGCAGTAACTCGGGCATCAGC 1057
Db 481 CTGATGGATAGTGCAGGCTGGCGCGCCCTGCCCCCAGCAGTAACTCGGGCATCAGC 540
QY 1058 GCCACGTGTACCGCAGCGCGCGCGCATGGAGGGCGCGCCGCCACCTACAGCGAGGTC 1117
Db 541 GCCACGTGTACCGCAGCGCGCGCGCATGGAGGGCGCGCCGCCACCTACAGCGAGGTC 600
QY 1118 ATCGGCCACTACCCGGGTCTCTCTTCCAGACACGACAGAGAGTGGGCCCTCTCTTG 1177
Db 601 ATCGGCCACTACCCGGGTCTCTCTTCCAGACACGACAGAGAGTGGGCCCTCTCTTG 660
QY 1178 CTGGAGGGGACCCCGCTCCACACACACATCGCGCCCCCTAGAGAGCGCAGCCATCTGG 1237
Db 661 CTGGAGGGGACCCCGCTCCACACACACATCGCGCCCCCTAGAGAGCGCAGCCATCTGG 720
QY 1238 AGCAAGAGAGGATAAACAAGAAAGGACACCCCTCTCTAG 1276
Db 721 AGCAAGAGAGGATAAACAAGAAAGGACACCCCTCTCTAG 759
```

Search completed: May 12, 2004, 08:24:15

Job time : 669.311 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2004, 00:10:42 ; Search time 3666.63 Seconds

(without alignments)
9944.945 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321

Sequence: 1 cgaccggctctcgagcga.....ctcgtagtggaaggcag 1321

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:**
2: em_esthum:**
3: em_estin:**
4: em_estmu:**
5: em_estov:**
6: em_estpl:**
7: em_estro:**
8: em_hcc:**
9: gb_est1:**
10: gb_est2:**
11: gb_hcc:**
12: gb_est3:**
13: gb_est4:**
14: gb_est5:**
15: em_estfun:**
16: em_estom:**
17: em_gss_hum:**
18: em_gss_inv:**
19: em_gss_pln:**
20: em_gss_vrt:**
21: em_gss_fun:**
22: em_gss_mam:**
23: em_gss_mus:**
24: em_gss_pro:**
25: em_gss_rod:**
26: em_gss_phg:**
27: em_gss_vrl:**
28: gb_gss1:**
29: gb_gss2:**

Result No.	Score	Query Match	Length	ID	Description
C 1	866	65.6	1201	9	AL517150
C 2	859.4	65.1	1009	9	AL578575
C 3	766.8	59.0	967	13	BQ641849
C 4	766	58.0	1046	12	BM922276

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	764.2	57.9	1201	9	AL543170
6	736.4	55.7	916	13	BQ954555
7	735	55.6	951	9	AL558881
8	715.4	54.2	1007	9	AL558882
9	715	54.1	874	13	BX362396
10	691.2	52.3	945	13	BX362396
11	686.6	52.0	850	13	BX362396
12	681	49.3	780	29	AY419334
13	630.6	47.7	1207	11	AK008976
14	618.6	46.8	1079	11	BQ015170
15	614.6	46.5	782	12	BQ015170
16	607.4	46.0	609	13	BQ367642
17	605.8	45.9	915	13	BX367642
18	592	44.8	888	13	BX367642
19	578.4	43.8	890	13	BX367642
20	570.4	43.2	973	13	BX367642
21	568.8	43.1	572	13	BX367642
22	567.4	43.0	729	13	BX367642
23	564.8	42.8	730	12	BM677602
24	563.2	42.6	728	13	BM677602
25	550	41.6	551	12	BM141979
26	529.8	40.1	894	12	BM141979
27	521	39.4	1068	13	BM141979
28	507	38.4	780	29	AY419335
29	501.6	38.0	588	12	BM483503
30	493.6	37.4	693	9	AI761441
31	493.4	37.4	655	13	BQ691705
32	487.6	36.9	646	29	CG784226
33	486	36.8	1400	12	BM559329
34	480.8	36.4	964	13	BM559329
35	478.6	36.2	1174	9	AL517151
36	477.6	36.2	646	13	BQ691705
37	476.4	36.1	651	14	CB554226
38	475.2	36.0	624	29	AY419336
39	473.4	35.8	1017	13	BX400248
40	468.8	35.5	1280	13	BQ691500
41	468	35.4	857	12	BQ323347
42	468	35.4	974	10	BB624904
43	465.8	35.3	744	13	BQ414421
44	461	34.9	763	12	BI646175
45	455.4	34.5	629	13	BU730650

ALIGNMENTS

RESULT 1
AL517150/c
LOCUS AL517150 Homo sapiens NEUROBLASTOMA Homo sapiens cdna clone linear EST 09-MAY-2003
DEFINITION CS0DA008YB23 3-PRIME, mRNA sequence.
ACCESSION AL517150
VERSION AL517150.2 GI:30492472
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
1 (bases 1 to 1201)
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:12780643.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9945.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DA008C12NP1&cluster=9945.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :


```

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DA008CA12NP1.
Location/Qualifiers
1..1201
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DA008YB23"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="vector: pCMVSPORT 6; 1st strand cDNA was primed
with a Noll-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

```

ORIGIN

Query Match.	65.6%	Score 866;	DB 9;	Length 1201;
Best Local Similarity	88.9%;	Pred. No. 7.8e-111;		
Matches	926;	Conservative	23;	Mismatches 91;
			Indels	2;
			Gaps	2;
Qy	280	GCCCGGCGAGCGGGGCGGCTCCCGCGCGCGCGCTCTCTGCATCGGGGCCCCAGCT	339	
Db	1157	SCCCSGSCCCCGTTTKSGCCSCSGSCCGGGSGCGGGGCTTCCCCCGGCGCTCBQG	1098	
Qy	340	CCGGSCCCCGGAGCCCCCCCCCGCGCGCGCCCGCGAGCCCCCGCGCCCGCGCGCGC	399	
Db	1097	TKGGGCGCGCTCCGGGSGRGGASCCCCWCGGAAAAAAAANAACSGRMNAAGGCG	1038	
Qy	400	CGCGCGCGCTCATGACACCGCTTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGCG	459	
Db	1037	CGCSCSGCNGTCMATACCGCTTGTTGGGGTCAACAGCACCGCGCGCGCGCGCGCG	979	
Qy	460	GCAGCCCAATCTCTCGCAGCTGCAACTGCAACGCTCTTTGTTCCAGAGCATGGAGAT	519	
Db	978	GCAGCCCAATTTCTCTCGCAGCTGCCACTGCAACGCTTTTGTTCAGAGCATGGAGAT	919	
Qy	520	CACGGAGCTGAGTTTGTTCAGATCATCATCATCTGTGTGTGTGTGTGTGTGTGTGTGT	579	
Db	918	CACGGAGCTGAGTTTGTTCAGATCATCATCATCTGTGTGTGTGTGTGTGTGTGTGTGT	859	
Qy	580	GGTATCAGGTCCTGTGAGCCTACTACAGCTCTGTGCACGGTCCTTCTCATCAGCCGCA	639	
Db	858	GGTATCAGGTCCTGTGAGCCTACTACAGCTCTGTGCACGGTCCTTCTCATCAGCCGCA	799	
Qy	640	CAGCCAGGGGCGGAGGAGAGATGCCTCTCTCTCAGAGGATGCTGTGGCCCTCGGA	699	
Db	798	CAGCCAGGGGCGGAGGAGAGATGCCTCTCTCTCAGAGGATGCTGTGGCCCTCGGA	739	
Qy	700	GAGCACAGTGTACGCAACGGAATCCAGAGCCGAGGTCTACGCCCGCTCTGGGCCAC	759	
Db	738	GAGCACAGTGTACGCAACGGAATCCAGAGCCGCA-GTCTACGCCCGCTCTGGGCCAC	680	
Qy	760	CGACCGCTGCGCTGCGCGCTTCCGCCAGCGGAGCGCTTCCACCGCTTCCAGCCAC	819	
Db	679	CGACCGCTGCGCTGCGCGCTTCCGCCAGCGGAGCGCTTCCACCGCTTCCAGCCAC	620	
Qy	820	CTATCCGTACTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTACAGCGGGA	879	
Db	619	CTATCCGTACTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTACAGCGGGA	560	
Qy	880	GGAGCCCCCACTTACAGGCGCCCTGCAACCTCGAGCTTCGGGACCCCGAGCAGCAGCT	939	
Db	559	GGAGCCCCCACTTACAGGCGCCCTGCAACCTCGAGCTTCGGGACCCCGAGCAGCAGCT	500	
Qy	940	GGAATGAACCGGAGTCCGTTGGCGGACCCCCAAACAGAACCATCTTCGACAGTGAACCT	999	
Db	499	GGAATGAACCGGAGTCCGTTGGCGGACCCCCAAACAGAACCATCTTCGACAGTGAACCT	440	
Qy	1000	GATGGATAGTCCAGGCTGGCGGCGCTCTGCCCCCCCCAGCAGTAACTCGGGCATCAGCGC	1059	
Db	439	GATGGATAGTCCAGGCTGGCGGCGCTCTGCCCCCCCCAGCAGTAACTCGGGCATCAGCGC	380	

Qy	1060	CACGTGCTACTGGCAGCGGGCGGCATGAGAGGGCCGCCGCCACCTACAGCGAGGTCAT	1119
Db	379	CAGTGTCTACTGGCAGCGGGCGGCATGAGAGGGCCGCCGCCACCTACAGCGAGGTCAT	320
Qy	1120	CGGCCCACTACC CGGGGTCTCTTC CAGACACCA GAGAGAGAGTG GGGCGCCCTCTTGCT	1179
Db	319	CGGCCCACTACC CGGGGTCTCTTC CAGACACCA GAGAGAGAGTG GGGCGCCCTCTTGCT	260
Qy	1180	GGAAGGGAC CCGGCTTCCA CACA CACATCG GGGCCCTTAGAGAGCGCAGCATCTGGAG	1239
Db	259	GGAAGGGAC CCGGCTTCCC CACA CA CAGTCTG GGGCCCTTAGAGAGCGCAGCATCTGGAG	200
Qy	1240	CAAAGAAGAGGATAA AAGAAAGAC ACCCTCTCT TAGGGTCTCC CAGAGGGGGCCGGGTGG	1299
Db	199	CAAGAGAGAGTAAC AGAAGAGCA CCCCCTCTCT TAGGGTCTCC CAGAGGGGGCCGGGTGG	140
Qy	1300	GGTGTGCGTAGGTGAAAAGGCAG	1321
Db	139	GGTGTGCGTAGGTGAAAAGGCAG	118
RESULT 2			
AL578575/c			
LOCUS	AL578575 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens		
DEFINITION	cDNA clone CSODK001YC24 3-PRIME, mRNA sequence.		
ACCESSION	AL578575		
VERSION	AL578575.2 GI:31316780		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1. (bases 1 to 1009) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)		
AUTHORS			
TITLE			
JOURNAL			
COMMENT	On Feb 16, 2001 this sequence version replaced gi:12942781. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9945.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSODK001BB12NP1&cluster=9945.r . Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paradise Avenue Genoscope sequence ID : CSODK001BB12NP1.		
FEATURES			
source	<p>1..1009</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="CSODK001YC24"</p> <p>/cell_type="HELA CELLS COT 25-NORMALIZED"</p> <p>/cell_line="HELA"</p> <p>/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"</p> <p>/note="1st strand cDNA was primed with a NotI-oligo(d)r primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT-6 vector. Library was normalized."</p>		
ORIGIN			
Query Match	65.1%; Score 859.4; DB 9; Length 1009;		
Best Local Similarity	97.7%; Pred. No. 6.3e-110;		
Matches	882; Conservative 9; Mismatches 10; Indels 2; Gaps 2;		
Qy	420	GCTGTGAGGGGTTCAACAGCACCGCCGGCCGGGGGAG-CGCATGTCTCTGCG	478
Db	1009	GCTGTGAGGGGTTCAACAGCACCGCCGGCCGGGGGAGCCCAATTCTCTGCG	950

QY 1117 CATCGGCACACTACCGGGGTCCTCTTCCAGCACACAGAGAGTGGGCGGCCCTCTCTT 1176
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 Db 314 CATCGGCACACTACCGGGGTCCTCTTCCAGCACACAGAGAGTGGGCGGCCCTCTCTT 255
 |||||
 QY 1177 GCTGAGGGGACCGCGGTCCACACACACATCGCCCTCAGAGAGCGCAGCCATCTG 1236
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 Db 254 GCTGAGGGGACCGCGGTCCACACACACATCGCCCTCAGAGAGCGCAGCCATCTG 195
 |||||
 QY 1237 GAGCAAGAGAGGATGAACAGAAAGACACCTCTCTAGGGTCCCCAGGGGGCGGGC 1296
 |||||
 Db 194 GAGCAAGAGAGGATGAACAGAAAGACACCTCTCTAGGGTCCCCAGGGGGCGGGC 135
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 QY 1297 TGGGGCTGCGTAGGTGAAGGCGAG 1321
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 Db 134 TGGGGCTGCGTAGGTGAAGGCGAG 110
 |||||

RESULT 8
 AL558882 1007 bp mRNA linear EST 31-MAY-2003
 LOCUS
 DEFINITION Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
 Homo sapiens cDNA clone CS0DJ015F12 5-PRIME, mRNA sequence.
 ACCESSION AL558882
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1007)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:12903838.
 COMMENT
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 9945.r For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DJ015DC06QPI&cluster=9945.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DJ015DC06QPI.
 Location/Qualifiers
 1..1007
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="CS0DJ015F12"
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 /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
 10-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES

source
 1..1007
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DJ015F12"
 /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
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 10-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 54.2%; Score 715.4; DB 9; Length 1007;
 Best Local Similarity 99.1%; Pred. No. 6.6e-90;
 Matches 738; Conservative 2; Mismatches 3; Indels 2; Gaps 2;
 QY 577 GTGTGTATCATCGTCTGCTGAGCCACTACAAAGTGTGTGACGGTCTTTCATGACGC 636
 |||||
 Db 62 GGATGTGATCATCGTCTGCTGAGCCACTACAAAGTGTGTGACGGTCTTTCATGACGC 121
 |||||
 QY 637 GCACAGCCAGGGCGGAGAGAGATGCCCTGTCTCAGAGAGATGCTGTGCGCCCTC 696
 |||||
 Db 122 GCACAGCCAGGGCGGAGAGAGATGCCCTGTCTCAGAGAGATGCTGTGCGCCCTC 181
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QY 697 GGAGAGCACAGTGTGAGGCAACGGAATCCAGAGCGCAGGTCCTACGCCCTCGGCC 756
 |||||
 Db 182 GGAGAGCACAGTGTGAGGCAACGGAATCCAGAGCGCA-GTCTACGCCCTCGGCC 240
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 Db 241 CACCGACCGCTGGCGGTCGCGCCCTTCGCCAGGGGAGCGCTTCCACCGCTTCAGCG 300
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 QY 817 CACCTATCGTACCTGTCAGCAGGATCGAOCCTGCGACCCACCATCTCGTCTCAGACGG 876
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 Db 301 CACCTATCGTACCTGTCAGCAGGATCGAOCCTGCGGCCACCATCTCGTCTCAGACGG 360
 |||||
 QY 877 GAGGAGCGCCACCCCTACCGGGCCCTCGACCCCTCCAGCTTCGGGACCCCGAGCAGCA 936
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 Db 361 GAGGAGCGCCACCCCTACCGGGCCCTCGACCCCTCCAGCTTCGGGACCCCGAGCAGCA 420
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 QY 937 GCTGGAACCTGAACCGGGAGTGGTGGCGCACCCCAACAGAACCATCTTCGACAGTGA 996
 |||||
 Db 421 GCTGGAACCTGAACCGGGAGTGGTGGCGCACCCCAACAGAACCATCTTCGACAGTGA 480
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 QY 997 CCGTATGATAGTGCAGGCTGGGGCGCCCTGCGCCCGCCAGCAGTAACTCGGGCATCAG 1056
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 Db 481 CCGTATGATAGTGCAGGCTGGGGCGCCCTGCGCCCGCCAGCAGTAACTCGGGCATCAG 540
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 QY 1057 CGCCACGTCTACCGCAGCGCGGGCGCATGGAGGGCGCGCCGCCACCTACAGCGAGGT 1116
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 QY 1117 CATCGGCACACTACCGGGGTCCTCTTCCAGCACACAGAGAGTGGGCGGCCCTCTT 1176
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 QY 1177 GCTGAGGGGACCGCGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTG 1236
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 Db 661 GCTGAGGGGACCGCGCTCCACACACACATCGCGCCCTTAGAGAGCGCA-SCATCTG 719
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 QY 1237 GAGCAAGAGAGAGTAAACAGAAAGACACCTCTCTAGGGTCCCCAGGGGGCGGGC 1296
 |||||
 Db 720 GAGCAAGAGAGAGTAAACAGAAAGACACCTCTCTAGGGTCCCCAGGGGGCGGGC 779
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 QY 1297 TGGGGCTGCGTAGGTGAAGGCGAG 1321
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 Db 780 TGGGGCTGCGTAGGTGAAGGCGAG 804
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RESULT 9
 BX362396/c 874 bp mRNA linear EST 05-MAY-2003
 LOCUS
 DEFINITION Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
 Homo sapiens cDNA clone CS0DJ014YN15 3-PRIME, mRNA sequence.
 ACCESSION BX362396
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 874)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 9945.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DJ014CG08NP1&cluster=9945.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DJ014CG08NP1.

FEATURES	Source	Location/Qualifiers	Sequence ID
Query Match	54.1%;	Score 71.5; DB 13; Length 874;	
Best Local Similarity	96.2%;	Pred. No. 7.3e-99;	
Matches	731; Conservative	16; Mismatches 11; Indels 2; Gaps 2;	
QY	563	ATGATGGTGATGGTGGTGGTGATC-ACGTGCTCTCTGAGCCACTACAAGCTGTCTGCACG 621	
Db	874	ATGATGGTGATGGTGGTGGTGATCTMCGTCTCTCTGAGCCATTACAGCTGTCTGCACG 815	
QY	622	GTCCCTTCATACGCGGCACACGACGAGGCGGAGAGAGATGCCCTGTCTCTCAAGG 681	
Db	814	GTCCCTTCATACGCGGCGACGACGAGGCGGAGAGAGATGCCCTGTCTCTCAAGG 755	
QY	682	ATGCTCTGTGGCCCTCGGAGAGACAGTGTACGCAACGGGAATCCAGAGCCGACGGTCTA 741	
Db	754	ATGCTCTGTGGCCCTCGGAGAGACAGTGTACGCAACGGGAATCCAGAGCCGCA-GTYTA 696	
QY	742	CGCCCGCGCTCGGCCACCGACCGCCCTGGCCGTCGCCGCCCTTCGCCCCAGGGAGCGCTT 801	
Db	695	CGCCCGCGCTTCGGCCACCGACCGCTGTGGCCGTCGCCGCCCTTTCGCCAGGGAGGCGCTT 636	
QY	802	CCACCGCTTCCAGCCCACTATCCGTACCTCCAGCAGAGATCGAAGTCCCAACCAAC 981	
Db	635	CCACCGCTTCCAGCCCACTATCCGTACNTGNAGNAGATNGACNTGCGGCCCACT 576	
QY	862	CTCGCTGTACAGCGGGAGGAGCCGCCACCTACAGGCGCCCTGCACCTCCAGCTTCG 921	
Db	575	CTCGCTGTACAGCGGGAGGAGCCGCCACCTACAGGCGCCCTGCACCTACAGCTTCG 516	
QY	922	GGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGGCGGCAACCCCAACAGAAC 981	
Db	515	GGACCCCGAGAGCAGCTGGAACTGAACCGGGAGTCGGTGGCGGCAACCCCAACAGAAC 456	
QY	982	CATCTTCGACAGTGACCTGATGGATAGTCGCAGAGCTGGGGGGCCCTGCCCGCCAGCAG 1041	
Db	455	CATCTTCGACAGTGACCTGATGGATAGTCGCAGAGCTGGGGGGCCCTGCCCGCCAGCAG 396	
QY	1042	TAACTCGGGCATACGGCCACGTGCTACGGCAGCGGGGGGCGCATGAGGGGGCGCGCCG 1101	
Db	395	TAACTCGGGCATACGGCCACGTGCTACGGCAGCGGGGGGCGCATGAGGGGGCGCGCCG 336	
QY	1102	CACCTACAGGAGGTATCGGCCACTACCCGGGGTCTCTCTTCAGACACAGCAGAGCAG 1161	
Db	335	CACCTACAGGAGGTATCGGCCACTACCCGGGGTCTCTCTTCAGACACAGCAGAGCAG 276	
QY	1162	TGGCGCGCCCTCTTGTCTCGAGGGGACCGGCTCCACACACATCGCGCCCTTAGA 1221	
Db	275	TGGCGCGCCCTCTTGTCTCGAGGGGACCGGCTCCACACACATCGCGCCCTTAGA 216	
QY	1222	GAGCGAGCCATCTGAGCAGAGAGAGGATATACAGAAAGGACACCTCTTAGGGTCC 1281	
Db	215	GAGCGAGCCATCTGAGCAGAAAGAGAGATATACAGAAAGGACACCTCTTAGGGTCC 156	
QY	1282	CCAGGGGGCGCGGCTGGGGCTGCGTAGGTGAAAGGCAG 1321	
Db	155	CCAGGGGGCGCGGCTGGGGCTGCGTAGGTGAAAGGCAG 116	

Db 365 CTTCCACCGCTTCAGCCACCTATCGTACCTGCGAGCAGAGATCGACCTGCGGCCAC 424
 Qy 859 CATCTCGTGTGACAGCGGGAGAGCCACCTACCTACAGGCGCCCTGCACCTCCAGCT 918
 Db 425 CATCTCGTGTGCGAGCGGGAGAGCCACCTACCTACAGGCGCCCTGCACCTCCAGCT 484
 Qy 919 TCGGACCCCGAGCAGCAGCTGGAACCTGAACCGGGAGTGGTGGCGCACCCCAACAG 978
 Db 485 TCGGACCCCGAGCAGCAGCTGGAACCTGAACCGGGAGTGGTGGCGCACCCCAACAG 544
 Qy 979 AACCATCTTCAGAGTACCTGATGATAGTGCACAGGTGGCGGCCCTGCCGCCAG 1038
 Db 545 AACCATCTTCAGAGTACCTGATGATAGTGCACAGGTGGCGGCCCTGCCGCCAG 604
 Qy 1039 CAGTAACCTCGGGCATCAGCGCCACCTGCTACGGCAGCGCGGGCGCATGAGAGGGCGGCC 1098
 Db 605 CAGTAACCTCGGGCATCAGCGCCACCTGCTACGGCAGCGCGGGCGCATGAGAGGGCGGCC 664
 Qy 1099 GCCCACCCTACAGCGAGGTGATCGGCACCTACCCGGGTCTCTCTCCAGCAGCAGAG 1158
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 Qy 1159 CAGTGGGGCGCCCT-CCTTGTCTGGAGGGAGCCCGGCTCCACACACACATCGCG-CCC 1216
 Db 725 CAGTGGGGCGCCCTCTCTGTCTGGAGGGAGCCCGGCTCCACACACACATCGTGGCCC 784
 Qy 1217 CTAGAGAGCGCAG-CATCTGAGCAAGAGAGGATAAA-----CAGAAAGGACACCCCTC 1271
 Db 785 CTAAGAGCGCAGCCCATCTGAGCAAGAGAGGATAAAACCCGAAAGGAGCACCCTTC 844
 Qy 1272 TCTAGGTCCTCCAGGGGGCGGGCTGGGGCTGGG 1306
 Db 845 TCTAGGTCCTCCAGGGGGGGCGCGGCTGGG 879

RESULT 11

BU602918
 LOCUS AGENCOURT_10016502 NIH_MGC_142 Homo sapiens cDNA clone
 DEFINITION IMAGE:6497853 5', mRNA sequence.

ACCESSION BU602918
 VERSION BU602918.1
 KEYWORDS GI:23254677
 SOURCE EST.

ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 850)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: NCI
 cDNA Library Preparation: Michael Brownstein Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LICM2679 row: i column: 22
 High quality sequence stop: 499.
 Location/Qualifiers

FEATURES

source

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 /clone="IMAGE:6497853"
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 /clone_lib="NIH MGC 142"
 /notes="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggcgcctcgcc); Double-stranded cDNA was

ORIGIN

Query Match 52.0%; Score 686.6; DB 13; Length 850;
 Best Local Similarity 96.9%; Pred. No. 6.5e-86;
 Matches 743; Conservative 0; Mismatches 19; Indels 5; Gaps 4;

Qy 559 GGTGATGATGTTGATGTTGTTGATACGTGCTGCTGAGCCACTCAAGTGTCTGC 618
 Db 1 GGTGATGATGTTGATGTTGTTGATACGTGCTGCTGAGCCACTCAAGTGTCTGC 60
 Qy 619 ACCTGCTCTTCATCAGCCGCGCAGCGGGGGAGAGAGATGCTCTGCTCAGA 678
 Db 61 ACCTGCTCTTCATCAGCGCGCAGCCAGCGGGGGAGAGAGATGCTCTGCTCAGA 120
 Qy 679 AGGATGCTGTGCTTCGGAGAGCAGTGTTCAGGCAACGGAATCCGAGCGCGAGGT 738
 Db 121 AGGATGCTGTGCTTCGGAGAGCAGTGTTCAGGCAACGGAATCCGAGCGCGAGGT 180
 Qy 739 CTAGCGCCCGCTCGGCCACCGCCGCTGGCGGTGGCCCTTCGCCAGCGGGAGCG 798
 Db 181 CTAGCGCCCGCTCGGCCACCGCCGCTGGCGGTGGCCCTTCGCCAGCGGGAGCG 240
 Qy 799 CTTCCACCGCTTCAGCCCACTATCCGCTGTCAGCAGAGATCGACTGCCACCCAC 858
 Db 241 CTTCCACCGCTTCAGCCCACTATCCGCTGTCAGCAGAGATCGACTGCCACCCAC 300
 Qy 859 CATCTCGTGTGACAGCGGGAGAGCCCGCCACCTACAGGCGCCCTGCACCTCCAGCT 918
 Db 301 CATCTCGTGTGAGAGGGAGAGCCCGCCACCTACAGGCGCCCTGCACCTCCAGCT 360
 Qy 919 TCGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTGGTGGCGCACCCCAACAG 978
 Db 361 TCGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTGGTGGCGCACCCCAACAG 420
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 Db 421 AACCATCTTCAGAGTACCTGATGATAGTGCACAGGTGGCGGCCCTGCCGCCAG 480
 Qy 1039 CAGTAACCTCGGGCATCAGCGCCACCTGCTACGGCAGCGCGGGCGCATGAGAGGGCGGCC 1098
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 Qy 1099 GCCCACCCTACAGCGAGGTGATCGGCACCTACCCGGGTCTCTCTCCAGCAGCAGAG 1158
 Db 541 GCCCACCCTACAGCGAGGTGATCGGCACCTACCCGGGTCTCTCTCCAGCAGCAGAG 600
 Qy 1159 CAGTGGGGCG-CCCTCCTCTGCTG-AGGGAGCCCGGCTCCACACACACATCGCGGCC 1216
 Db 601 CAGTGGGGCGCCCTCTCTTCTGAGAGGGAGCCCGGTTCCACACACACAAATCGGGCCC 660
 Qy 1217 CTAGAGAGCGCAGCCA-TCTGGAGCAAGAGAGGATAAACAGAAAGGACACCCCTCTCTA 1275
 Db 661 CTAAGAGCGCAGCCATTCTGGAGCAGCAGAGATGATAAACCCGAAAGGAGACCCCTCTCTA 720
 Qy 1276 GGCTCCCCAGGGGGGCC--GGGCTGGGGCTGCGTGTGTAAGGGA 1320
 Db 721 GGCTCCCCAGGGGGGGCCCGGGCTGGGGGCTGTCTAGTGTGAAAGGA 767

prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
 5'-AAGCATGTTGTTATCAACGAGTGGCATTCATTACGGCGGG-3' and
 5'-ATTCTAGAGCGAGCGCGCCGACATG-dt(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH MGC 141). Library created in the laboratory of M. Brownstein (NIH, NIH). Note: this is a NIH MGC Library."


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RESULT 12
AY419334
LOCUS
DEFINITION Homo sapiens TM6PAI gene, GSS 17-DEC-2003
GENOMIC SURVEY SEQUENCE.
ACCESSION AY419334
VERSION AY419334.1 GI:39775291
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 780)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferris,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 780)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferris,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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ORIGIN
Query Match 49.3%; Score 651; DB 29; Length 780;
Best Local Similarity 86.2%; Pred. No. 5.7e-81;
Matches 551; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 522 CGGAGCTGGATTGTTTCAGATCATCATCATCGTGGTGGTATGATGATGATGATGATG 581
DB 26 CGGAGCTGGATTGTTTCAGATCATCATCATCGTGGTGGTATGATGATGATGATG 85
QY 582 TGATCAGTGGCTGCTGAGCCACTACAGCTGTCTGCACGCTCTTTCATCAGCGGCACA 641
DB 86 TGATCAGTGGCTGCTGAGCCACTACAGCTGTCTGCACGCTCTTTCATCAGCGGCACA 145
QY 642 GCCAGGGCGGAGGAGAGAGATGCTTCTCCTCAGAGGATGCTTGGCCCTCGGAGA 701
DB 146 GCCAGGGCGGAGGAGAGAGATGCTTCTCCTCAGAGGATGCTTGGCCCTCGGAGA 205
QY 702 GCACAGTGTACGGAACCGATCCAGCGCGCAGGTCTACGCCCTCGGCCACCG 761
DB 206 GCACAGTGTACGGAACCGATCCAGCGCGCAGGTCTACGCCCTCGGCCACCG 265
QY 762 ACCGCTGCGGCTGCGGCCCTTCGCCACGCGGAGCGCTTCACCGCTTCACGCCACCT 821
DB 266 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 325
QY 822 ATCCGTACTCGACGACGAGATCGACCTGCCACCCACCATCTCCTGTTCAGCGGAGG 881
DB 326 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 385
QY 882 AGCCCCACCTTACCGAGGCGCCCTGACCCCTCCAGTTCGGAGCCCGGAGCAGAGCTGG 941
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QY 942 AACTGAACGGGAGTCGTGCGCGCACCCCCAAACAGAACCATCTTTCAGAGTGACCTGA 1001
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QY 1002 TGGATAGTGCAGGCTGGCGGCCCTCCCTCCAGACACGAGTAACTTCGGGCGATCAGCGCA 1061
DB 506 TGGATAGTGCAGGCTGGCGGCCCTCCCTCCAGACACGAGTAACTTCGGGCGATCAGCGCA 565
QY 1062 COTGCTACGGCAGCGCGGCGCATGAGAGGGCGCGCCGCCACCTTACAGGAGGTCATCG 1121
DB 566 COTGCTACGGCAGCGCGGCGCATGAGAGGGCGCGCCGCCACCTTACAGGAGGTCATCG 625
QY 1122 GCACCTACCCGGGGTCCCTTCCAGACACGAGTGGCGGCCCTCCCTTCCTTGGCTGG 1181
DB 626 GCACCTACCCGGGGTCCCTTCCAGACACGAGTGGCGGCCCTCCCTTCCTTGGCTGG 685
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RESULT 13
AK008976
LOCUS
DEFINITION Mus musculus adult male stomach cDNA, RIKEN full-length enriched
library, clone:210418102 product:Need4 WW binding protein 4, full
insert sequence.
ACCESSION AK008976
VERSION AK008976.1 GI:12843488
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci,P. and Hayashizaki,Y.
AUTHORS High-efficiency full-length cDNA cloning
TITLE Meth. Enzymol. 303, 19-44 (1999)
JOURNAL 99279253
MEDLINE
PUBMED 10349636
2
Carninci,P. and Hayashizaki,Y.
AUTHORS Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
TITLE Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL 20499374
MEDLINE
PUBMED 11042159
3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuana,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,T., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE
PUBMED 11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
AUTHORS Functional annotation of a full-length mouse cDNA collection
TITLE Nature 409, 685-690 (2001)
JOURNAL
PUBMED
REFERENCE 5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.

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/note="Organ: Left Pubic Bone; Vector: pT73-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C85. The library was constructed according to
Bonald, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dr primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CCTCAAGGCT.
TAG_TISSUE=chondrosarcoma
TAG_LIIB=UI-H-SD1
TAG_SEQ=CGTCAAGGCT"

ORIGIN

	Query Match	46.5%	Score 614.6;	DB 12;	Length 782;
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QY	758	ACCGACCGCTGGCGCTGGCGCCCTTCGCCCGCAGCGGAGCGCTCCACCGCTTCAGGCC	817		
Db	722	ACCGACCGCTGGCGCTGGCGCCCTTCGCCCGCAGCGGAGCGCTTCACCGCTTCAGGCC	663		
QY	818	ACCTATCCGTACTCTCAGCAGCAGATCGACCTGCCACCCACCATCTCGCTGTCTCAGACGG	877		
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QY	1058	GCCAGTGTCTAGCGCAGCGCGGCGCATGTGAGGGGCGCGCCGCCACCTACAGCGAGGTC	1117		
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QY	1118	ATCGGCCACTACCCGGGGTCTCTTCCAGCACACAGAGAGCAGTGGGCGCGCCCTTCCTTG	1177		
Db	362	ATCGGCCACTACCCGGGGTCTCTTCCAGCACACAGAGAGCAGTGGGCGCGCCCTTCCTTG	303		
QY	1178	CTGGAGGGACCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCATCTGG	1237		
Db	302	CTGGAGGGACCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCATCTGG	243		
QY	1238	AGCAAGAGAGAGATAAACAGAAAGACACCTCTCTAGGGTCCCCAGGGGGCGGGCT	1297		
Db	242	AGCAAGAGAGAGATAAACAGAAAGACACCTCTCTAGGGTCCCCAGGGGGCGGGCT	183		
QY	1298	GGGGTGCCTAGGTGAAAGGGCAG	1321		
Db	182	GGGGTGCCTAGGTGAAAGGGCAG	159		

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